

GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: April 3, 2006, 05:30:20 ; Search time 23 Seconds
(without alignment)

1008.184 Million cell updates/sec

Title: US-09-979-539-1

Perfect score: 1276

Sequence: 1 MOVQLQSGSPLEKPKGASVK.....CQMSGYPLTFAGTKLEIK 241

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 9621673 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR 80:*

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	850.5	66.7	268	2	A56446 Ig heavy chain V r
2	733	57.4	249	2	S41374 single chain Fv an
3	663	52.0	233	2	JC5322 p53 specific singl
4	529	41.5	144	2	B30502 Ig heavy chain V r
5	516.5	40.5	122	2	PH0887 Ig heavy chain V r
6	513.5	40.2	137	2	H32513 Ig heavy chain pre
7	503.5	39.5	120	2	E45722 anti-glycoprotein
8	502	39.3	130	1	JL0079 Ig kappa chain pre
9	501.5	39.3	119	2	F30502 Ig heavy chain V r
10	501	39.3	119	2	PH0099 Ig heavy chain V r
11	500.5	39.2	114	2	S26319 Ig heavy chain V r
12	499	39.1	103	2	S29591 Ig kappa chain V r
13	499	39.1	107	2	A30562 Ig kappa chain V r
14	496.5	38.9	120	2	F45722 anti-glycoprotein
15	496	38.9	107	2	B30562 Ig kappa chain V r
16	496	38.9	107	2	PC4405 Ig kappa chain pre
17	495.5	38.8	135	2	PS0057 Ig heavy chain V r
18	495	38.8	104	2	B49049 Ig kappa chain V r
19	495	38.8	106	2	PS0071 Ig kappa chain V r
20	495	38.8	235	2	S25058 Ig kappa chain - m
21	493.5	38.7	128	2	I37267 Ig heavy chain V r
22	492.5	38.6	118	1	MHMS38 Ig heavy chain V r
23	491.5	38.5	128	2	C37267 Ig heavy chain V r
24	487	38.2	119	2	B53285 Ig heavy chain V a
25	487	38.2	125	2	PH0100 Ig heavy chain V r
26	482.5	37.8	139	2	A27609 Ig heavy chain pre
27	482	37.8	107	2	S11119 Ig kappa chain V r
28	482	37.8	107	2	PT0398 Ig light chain V r
29	481.5	37.7	112	2	S09957 Ig heavy chain V-D

30	481	37.7	107	2	S11118 Ig kappa chain V r
31	478	37.5	107	2	PT0402 Ig light chain V r
32	478	37.5	107	2	S11121 Ig kappa chain V r
33	478	37.5	117	1	MHMS4E Ig heavy chain V r
34	478	37.5	117	1	MHMSJ5 Ig heavy chain V r
35	478	37.5	140	2	T01407 Ig heavy chain (my
36	475	37.2	106	2	G27887 Ig kappa chain V r
37	474	37.1	107	2	PD0011 Ig kappa chain V r
38	474	37.1	120	2	A34871 Ig kappa chain V r
39	473.5	37.1	108	2	G30560 Ig kappa chain V r
40	473	37.1	107	2	PT0406 Ig kappa chain V r
41	472.5	37.0	120	2	A49982 Ig heavy chain V r
42	472.5	37.0	128	2	A37267 Ig heavy chain V r
43	472	37.0	107	2	PT0403 Ig light chain V r
44	471	36.9	118	2	PI0200 anti-DNA autoantib
45	470	36.8	100	2	S29590 Ig kappa chain V r

ALIGNMENTS

```
RESULT 1
A56446
Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)
C/Date: 19-Jan-1996 #sequence #revision 19-Jan-1996 #text_change 16-Aug-1996
C/Accession: A56446
J.Tang, P.M.; Poltz, L.A.; Mahoney, W.C.; Schueler, P.A.
J. Biol. Chem. 270, 7829-7835, 1995
A/Title: A high affinity digoxin-binding protein displayed on M13 is functionally iden
A/Reference number: A56446; MUID:95229583; PMID:7713873
A/Accession: A56446
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-268 <TAN>
A/Cross-references: UNIPARC:UPI000017C6D0; GB:U20617
C/Keywords: heterotetramer; immunoglobulin

Query Match      66.7%; Score 850.5; DB 2; Length 268;
Best Local Similarity 69.6%; Pred. No. 4,6e-49;
Matches 167; Conservative 25; Mismatches 47; Indels 1; Gaps 1;

QY      2 QVQLQSGSPLEKPKGASVKLSCKASGYFTGTMNWVQSHKSLSEWIGLTPVNGASY 61
      3 QVQLQSGSPLEKPKGASVKLSCKASGYFTGTMNWVQSHKSLSEWIGLTPVNGASY 61
DB      62 NOKFRGKATLTVDKSSSTAYMDLSTLTSDESAVYFCARGYDGRGFDYWGQTTVTSSG 121
      63 DKPFGKATLTADTSSNTAYTQLSLTSDEDAVYCA-SYILTRYENTWGQTTVTSSG 121
QY      122 VGGSGGGSGGGGSDILTQSPAIMSASPGKVTWTCASSSVSYMHVYQKSGTSPKRW 181
      122 GGGSGGGSGGGGSDILTQSPAIMSASLGEKVTWTCASSSVNFIYWYQKSDASPKLW 181
DB      122 IYDTSKLASGVDPGRSGSGSGSYSLTTSVEARDDARYVCOQMSGYPLTFAGTKLEIK 241
      122 VYTTSHLPVPVAPRPSGSGSNYSYLTTSMEGEDAATYVCOQFTSSPTFGSKLEIK 241
QY      162 IYDTSKLASGVDPGRSGSGSGSYSLTTSVEARDDARYVCOQMSGYPLTFAGTKLEIK 241
      162 VYTTSHLPVPVAPRPSGSGSNYSYLTTSMEGEDAATYVCOQFTSSPTFGSKLEIK 241

RESULT 2
S41374
single chain Fv antibody - mouse
C/Species: Mus musculus (house mouse)
C/Date: 06-Jan-1995 #sequence #revision 06-Jan-1995 #text_change 06-Jan-1995
C/Accession: S41374
R.Abrahamko, O.; Weiler, E.W.; Muentz, K.; Conrad, U.
submitted to the EMBL Data Library, January 1994
A/Description: Construction and functional characterization of a single chain Fv antib
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-249 <ART>
```

A:Cross-references: UNIPARC:UPI000017C74A; EMBL:229480

Query Match 57.4%; Score 733; DB 2; Length 249;
Best Local Similarity 60.6%; Pred. No. 2.2e-41;
Matches 149; Conservative 27; Mismatches 64; Indels 6; Gaps 1;

```
QY 2 QVQLQSGPELEKPGASVYLSCKASGYSTGYTMVMVKSHGKSLIEWIGLITPYNGASSY 61
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVQLQSGPELEKPGASVYLSCKASGYSTGYTMVMVKSHGKSLIEWIGLITPYNGASSY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 62 NQKFRGKATLVYDKSSSTAYMDLLSTSEDSAVYFCARGGYDGRGPDYWGQGTITVYSSG 121
   :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 VRFQDKATITADTSNTAYLLSLTSEDTAVYCARDDTYLTSIGYWGQSTVTVSSR 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 122 VGGSGGGSGGGGSDIELTQSPALMSAPGEKVTMTCSASSV-----SYMHVYQQKSG 175
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 GGGSGGGSGGGGSDIELTQSPSPVYVIGESVYSISCRSSKSLVSDGDSYLFMFILQRP 180
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 176 TSPKRWITPYSKLASGVPGRFSGSGGNSYSLTISVVEAEDATYTCQWMSGYPLTFGAG 235
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 QSPOLLITRYMSNLASGVPDRFSGSGGTFILRIKVEAEDVGVYVCMQHREYPLTFGAG 240
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 236 TKLEIK 241
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 TKLEIK 246
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

RESULT 3

JCS322 p53 specific single-chain antibody Fab421 - human

C:Species: Homo sapiens (man)
C:Date: 15-May-1997 #sequence_revision 15-May-1997 #text_change 18-Jul-1997

C:Accession: JCS322
R:Janot, C.B.; Hynes, N.E.

Biochem. Biophys. Res. Commun. 230, 242-246, 1997

A:Title: Characterization of scFv-421, a single-chain antibody targeted to p53.

A:Reference number: JCS322; MUID:97168950; PMID:9016757

A:Accession: JCS322

A:Molecule type: mRNA

A:Residues: 1-233 <JAN>

A:Cross-references: UNIPARC:UPI000017C2DE

A:Experimental source: hydricioma cell

C:Comment: This protein specifically binds the tumor suppressor protein p53. It restores

Query Match 52.0%; Score 663; DB 2; Length 233;

Best Local Similarity 57.5%; Pred. No. 8.1e-37;

Matches 138; Conservative 24; Mismatches 66; Indels 12; Gaps 3;

```
QY 6 QQSGPELEKPGASVYKLSCKASGYSTGYTMVMVKSHGKSLIEWIGLITPYNGASSYNOKF 65
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QQSGPELEKPGASVYKLSCKASGYSTGYTMVMVKSHGKSLIEWIGLITPYNGASSYNOKF 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 66 RGAATLVYDKSSSTAYMDLLSTSEDSAVYFCARGGYDGRGPDYWGQGTITVYSSGSGS 125
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 GYKATITADTSNTAYLLSLTSEDTAVYTC-----NAGMDYWGQGTITVYSSGSGS 114
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 126 GGGSGGGSGGGSDIELTQSPALMSAPGEKVTMTCSASSV-----SYMHVYQQKSGTSPR 180
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 115 GGAASCGGSDIELTQSPALMSAVSLGATATISCRASKSVTSGSYGMHNNQKPGQPPRL 174
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 181 WYDTKSLASGVGRSSGSGNSYSLTISVVEAEDATYTCQWMSGYPLTFGAGTKLEI 240
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 175 LYLVLNLSGVPARFSGSGGTFDLNIHPVEEADATYTCQHRELTRSRG-GTKLEI 233
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

RESULT 4

B30502 Ig heavy chain V region (D444) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 03-Nov-1988 #sequence_revision 03-Nov-1988 #text_change 21-Jan-2000

C:Accession: B30502

R:Blatt, D.; Webster, D.M.; Rees, A.R.

J. Immunol. 141, 1745-1753, 1988

A:Title: V region sequences of anti-DNA and anti-RNA autoantibodies from NZB/NZW F-1 mice

A:Reference number: A30502; MUID:86315787; PMID:2457627

A:Accession: B30502

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-144 <ELL>

A:Cross-references: UNIPARC:UPI0000176D4C

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 41.5%; Score 529; DB 2; Length 144;
Best Local Similarity 63.2%; Pred. No. 3.1e-28;
Matches 103; Conservative 16; Mismatches 22; Indels 22; Gaps 2;

```
QY 2 QVQLQSGPELEKPGASVYKLSCKASGYSTGYTMVMVKSHGKSLIEWIGLITPYNGASSY 61
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVQLQSGPELVKPGASVYKLSCKASGYSTGYTMVMVKSHGKSLIEWIGLITPYNGASTY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 62 NQKFRGKATLVYDKSSSTAYMDLLSTSEDSAVYFCARGGYDGRGPDYWGQGTITVYSSG 121
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 NEKFRGKATLVYDKSSSTAYMDLLSTSEDSAVYFCARGGYDGRGPDYWGQGTITVYSSG 112
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 122 VGGSGGGSGGGGSDIELTQSPALMSAPGEKVTMTCSASSV 164
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 113 -----DILITQSPALISVSPGRVSFSCASQSI 141
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

RESULT 5

PH0887 Ig heavy chain V region (anti-CD3) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 21-Jan-2000

C:Accession: PH0887

R:Shalaby, M.R.; Shepard, H.M.; Presta, L.; Rodrigues, M.L.; Beverley, P.C.L.; Feldmann

J. Exp. Med. 175, 217-225, 1992

A:Title: Development of humanized bispecific antibodies reactive with cytotoxic lymphoc

A:Reference number: PH0885; MUID:92113462; PMID:1346155

A:Accession: PH0887

A:Molecule type: mRNA

A:Residues: 1-122 <SHA>

A:Cross-references: UNIPARC:UPI0000176B39

A>Note: the authors translated the codon TTC for residue 70 as Leu

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 40.5%; Score 516.5; DB 2; Length 122;
Best Local Similarity 80.3%; Pred. No. 1.7e-27;
Matches 98; Conservative 9; Mismatches 12; Indels 3; Gaps 1;

```
QY 2 QVQLQSGPELEKPGASVYKLSCKASGYSTGYTMVMVKSHGKSLIEWIGLITPYNGASSY 61
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVQLQSGPELVKPGASVYKLSCKASGYSTGYTMVMVKSHGKSLIEWIGLITPYNGASTY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 62 NQKFRGKATLVYDKSSSTAYMDLLSTSEDSAVYFCARGGYDGRG---FDYWGQGTITVY 118
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 NQKFRGKATLVYDKSSSTAYMDLLSTSEDSAVYFCARGGYDGRG---FDYWGQGTITVY 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 119 SS 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 SS 122
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

RESULT 6

H32513 Ig heavy chain precursor V region (BXW16) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000

C:Accession: H32513

R:Kofler, R.; Ströhal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.;

J. Clin. Invest. 82, 852-860, 1988

A:Title: Immunoglobulin kappa light chain variable region gene complex organization an

A:Reference number: A94689; MID:88331394; PMID:3138286
A:Accession: H32513
A:Molecule type: DNA
A:Residues: 1-137 <R0F>
A:Cross-references: UNIPARC:UPI00001149A; GB:M20831; NID:g196949; PIDN:AAA38848.1; PID:
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 40.2%; Score 513.5; DB 2; Length 137;
Best Local Similarity 82.4%; Pred. No. 3.1e-27;
Matches 98; Conservative 8; Mismatches 12; Indels 1; Gaps 1;

QY 2 QVLOOQSGPELEKPGASVSKSCASGYSFTGYTMNWKSHGKSLWIGLITPYNGASSY 61
DB 20 EIQLOOQSGPELEKPGASVSKSCASGYSFTGYTMNWKSHGKSLWIGLITPYNGASTY 79

QY 62 NQKFGKATLTVYDKSSSTAYMDLSLTSEDSAVYFCARGGYDGRGPDYWGQGTITVSS 120
DB 80 NQKFGKATLTVYDKSSSTAYMDLSLTSEDSAVYFCARGGYDGRGPDYWGQGTITVSS 137

RESULT 7
E45722
anti-glycoprotein H monoclonal antibody heavy-chain variable domain (Mab 5) - mouse (fr
C:Species: Mus musculus (house mouse)
C>Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: E45722
R:Simpon, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vasequ
J. Virol. 67, 489-496, 1993
A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on hu
A:Reference number: A45722; MID:93100833; PMID:7677958
A:Accession: E45722
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-120 <SIM>
A:Cross-references: UNIPARC:UPI0000176DAE
A:Note: Sequence extracted from NCBI backbone (NCBI:P120593)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: glycoprotein
F:15-99/Domain: immunoglobulin homology <IMM>

Query Match 39.5%; Score 503.5; DB 2; Length 120;
Best Local Similarity 79.2%; Pred. No. 1.2e-26;
Matches 95; Conservative 12; Mismatches 12; Indels 1; Gaps 1;

QY 2 QVLOOQSGPELEKPGASVSKSCASGYSFTGYTMNWKSHGKSLWIGLITPYNGASSY 60
DB 1 EVOLOOQSGPELEKPGASVSKSCASGYSFTGYTMNWKSHGKSLWIGLITPYNGASTS 60

QY 61 YNOKFGKATLTVYDKSSSTAYMDLSLTSEDSAVYFCARGGYDGRGPDYWGQGTITVSS 120
DB 61 YNOKFGKATLTVYDKSSSTAYMDLSLTSEDSAVYFCARGGYDGRGPDYWGQGTITVSS 120

RESULT 8
JL0079
Ig kappa chain precursor V region (anti-phenylloxazalone 6F6) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 31-Dec-1991 #sequence_revision 09-Aug-1996 #text_change 16-Jul-1999
C:Accession: JL0079; A49044; B49044
R:Kaartinen, M.; Rocca-Serra, J.; Maekela, O.
Mol. Immunol. 25, 859-865, 1988
A:Title: Combinatorial association of V genes: one VH gene codes for three non-cross-rea
A:Reference number: JL0076; MID:89096973; PMID:3211160
A:Accession: JL0079
A:Molecule type: mRNA
A:Residues: 1-130 <R0A>
A:Cross-references: UNIPARC:UPI000017371F; GB:M27792; NID:g197159
A:Experimental source: mRNA clones for anti-phenylloxazalone antibody 6F6
A:Note: the authors translated the codon TTC for residue 8 as Pro and TTC for residue 10
A:Note: the codon given for 1-Met (AGT) is inconsistent with the authors' translation
R:Miller, C.; Even, J.; Jarvis, J.M.; Gonzalez-Fernandez, A.; Gherardi, E.

Eur. J. Immunol. 22, 1627-1634, 1992
A:Title: Non-random features of the repertoire expressed by the members of one V kappa
A:Reference number: A49044; MID:92289826; PMID:1601044
A:Accession: A49044
A:Molecule type: DNA
A:Residues: 1-25 <MIL>
A:Cross-references: UNIPARC:UPI000011760C; GB:S37664; NID:g250215; PIDN:AA822332.1; PI
A:Note: sequence extracted from NCBI backbone (NCBIN:106807, NCBI:P106807)
A:Accession: B49044
A:Molecule type: DNA
A:Residues: 114-116 <MIL2>
A:Cross-references: UNIPARC:UPI00001188E5; GB:S37664; NID:g250215; PIDN:AA822332.1; PI
A:Experimental source: BALB/c germ-line
A:Note: sequences extracted from NCBI backbone, partial nucleotide sequences of 13 add
C:Genetics:
A:Gene: V(kappa)Ox1
A:Introns: 17/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (k
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-130/Product: Ig kappa chain V region (6F6) #status predicted <MAT>
F:38-111/Domain: immunoglobulin homology <IMM>
F:45-109/Disulfide Bonds: #status predicted

Query Match 39.3%; Score 502; DB 1; Length 130;
Best Local Similarity 92.4%; Pred. No. 1.6e-26;
Matches 97; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 137 IELTSPAIMSAPBEKTYMTCSASSSVYMMYQKSGTSKRYITTSKASGVPARF 196
DB 24 IYLTSPAIMSAPBEKTYMTCSASSSVYMMYQKSGTSKRYITTSKASGVPARF 83

QY 197 SSGSGNSYSLTSSVBAEDATYCCQWMSGPLTFGAGTKLEIK 241
DB 84 SSGSGNSYSLTSSVBAEDATYCCQWMSGPLTFGAGTKLEIK 128

RESULT 9
F30502
Ig heavy chain V region (A52) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 03-Nov-1988 #sequence_revision 03-Nov-1988 #text_change 21-Jan-2000
C:Accession: F30502
R:Blatt, D.; Webster, D.M.; Rees, A.R.
J. Immunol. 141, 1745-1753, 1988
A:Title: V region sequences of anti-DNA and anti-RNA autoantibodies from NZB/NZW F-1 m
A:Reference number: A30502; MID:8815787; PMID:2457627
A:Accession: F30502
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-119 <EIL>
A:Cross-references: UNIPARC:UPI0000176B33
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 39.3%; Score 501.5; DB 2; Length 119;
Best Local Similarity 78.9%; Pred. No. 1.6e-26;
Matches 97; Conservative 9; Mismatches 8; Indels 9; Gaps 2;

QY 2 QVLOOQSGPELEKPGASVSKSCASGYSFTGYTMNWKSHGKSLWIGLITPYNGASSY 61
DB 1 EIQLOOQSGPELEKPGASVSKSCASGYSFTGYTMNWKSHGKSLWIGLITPYNGASTY 60

QY 62 NQKFGKATLTVYDKSSSTAYMDLSLTSEDSAVYFCAR-----RGYDGRGPDYWGQGTITV 116
DB 61 NQKFGKATLTVYDKSSSTAYMDLSLTSEDSAVYFCARGLRGRGY----FDYWGQGTITL 116

QY 117 TTS 119
|||

Db 117 TWS 119

RESULT 10

Ig heavy chain V region (anti-cyclosporin F) - mouse (fragment)

C/Species: Mus musculus (house mouse)
C/Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 21-Jan-2000

C/Accession: PH0099

R/Schmitter, D.; Poch, O.; Zeder, G.; Heinrich, G.F.; Kocher, H.P.; Quesniaux, V.F.J.; V Mol. Immunol. 27, 1029-1038, 1990

A/Title: Analysis of the structural diversity of monoclonal antibodies to cyclosporine.
A/Reference number: PH0087; MID:91042649; PMID:2122240

A/Accession: PH0099

A/Molecule type: mRNA

A/Residues: 1-119 <SCH>

A/Cross-references: UNIPARC:UPI0000176847
C/Suprafamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/15-98/Domain: immunoglobulin homology <IMM>
F/31-35/Region: complementarity-determining 1
F/50-66/Region: complementarity-determining 2
F/99-106/Region: complementarity-determining 3Query Match 39.3%; Score 501; DB 2; Length 119;
Best Local Similarity 80.7%; Pred. No. 1.7e-26;
Matches 96; Conservative 11; Mismatches 10; Indels 2; Gaps 1;

QY 2 OYLOOOSPELEKPGAVKLSCKASGYSGFTGMNWKSHGKSLWIGLITPPYNGASSY 61

Db 1 EVQLOOSPELVKPGASMKISCKASYSFAGTMTWVSKHGNLWIGLITPPYDSIAT 60

QY 62 NQKFRKATLVYDKSSSTAYMDLSTLSDSAVYFCARGGYDGRGFTVYGGTTVYSS 120

Db 61 NQKFRKATLVYDKSSSTAYMDLSTLSDSAVYFCARGGY--YAVDYGQGTSTVYSS 117

RESULT 11

Ig heavy chain V region - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 21-Jan-2000

C/Accession: S26319

R/Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991A/Title: Antibodies that are specific for a single amino acid interchange in a protein
A/Reference number: S26309; MID:91341421; PMID:1908510

A/Accession: S26319

A/Molecule type: mRNA

A/Residues: 1-114 <STA>

A/Cross-references: UNIPARC:UPI0000176948; EMBL:X59172
C/Suprafamily: immunoglobulin V region; immunoglobulin homologyC/Keywords: heterotetramer; immunoglobulin
F/11-94/Domain: immunoglobulin homology <IMM>Query Match 39.2%; Score 500.5; DB 2; Length 114;
Best Local Similarity 82.6%; Pred. No. 1.8e-26;
Matches 95; Conservative 8; Mismatches 11; Indels 1; Gaps 1;

QY 6 OOSGPELEKPGAVKLSCKASGYSGFTGMNWKSHGKSLWIGLITPPYNGASSY 65

Db 1 OOSGPELVKPGASVKISCKASGYSGFTGMNWKSHGKSLWIGLITPPYNGTTVYNOKF 60

QY 66 RGRATLVYDKSSSTAYMDLSTLSDSAVYFCARGGYDGRGFTVYGGTTVYSS 120

Db 61 KGRATLVYDKSSSTAYMDLSTLSDSAVYFCARGGYDGRGFTVYSS 114

RESULT 12

S29591

Ig kappa chain V region - mouse

C/Species: Mus musculus (house mouse)

C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000

C/Accession: S29591

R/Kavaler, J.

Submitted to the EMBL Data Library, April 1991

A/Reference number: S26459

A/Accession: S29591

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-103 <KAV>

A/Cross-references: UNIPARC:UPI0000115F57; EMBL:X59094; MID:952227; PIDN:CAA41820.1; PI

C/Suprafamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin
F/15-88/Domain: immunoglobulin homology <IMM>Query Match 39.1%; Score 499; DB 2; Length 103;
Best Local Similarity 93.2%; Pred. No. 2e-26;
Matches 96; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 137 IELTQSPAIMSASPEKVTMTCSASSSVYHMYQOKSGTSPKRWYDTSKLASGVGRF 196

Db 1 IYLTQSPAIMSASPEKVTMTCSASSSVYHMYQOKSGTSPKRWYDTSKLASGVPARF 60

QY 197 SSGSGNSYSLTSSVEAEDDATYCCQMSGYPITFGAGTYKE 239

Db 61 SSGSGTSTLSSMEAEADATYCCQMSNPITFGAGTYKE 103

RESULT 13

Ig kappa chain V regions (27.7.2 and 27.4b.2) - mouse

C/Species: Mus musculus (house mouse)

C/Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 21-Jan-2000

C/Accession: A30562

R/Sikder, S.K.; Borden, P.; Gruezo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison, S.
J. Immunol. 142, 888-893, 1989A/Title: Amino acid substitutions in V-H CDR2 change the idiotype but not the antigen-b
A/Reference number: A30562; MID:89110066; PMID:2464031

A/Accession: A30562

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-107 <SIK>

A/Cross-references: UNIPARC:UPI00001767B0
C/Suprafamily: immunoglobulin V region; immunoglobulin homologyC/Keywords: heterotetramer; immunoglobulin
F/16-89/Domain: immunoglobulin homology <IMM>Query Match 39.1%; Score 499; DB 2; Length 107;
Best Local Similarity 91.4%; Pred. No. 2.1e-26;
Matches 96; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 137 IELTQSPAIMSASPEKVTMTCSASSSVYHMYQOKSGTSPKRWYDTSKLASGVGRF 196

Db 2 IYLTQSPAIMSASPEKVTMTCSASSSVYHMYQOKSGTSPKRWYDTSKLASGVPARF 61

QY 197 SSGSGNSYSLTSSVEAEDDATYCCQMSGYPITFGAGTYKE 241

Db 62 SSGSGTSTLSSMEAEADATYCCQMSNPYFGGTYKEIK 106

RESULT 14

anti-glycoprotein H monoclonal antibody heavy-chain variable domain (Mab 33) - mouse (f

C/Species: Mus musculus (house mouse)

C/Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000

C/Accession: F45722

R/Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vase

J. Vitrol. 67, 489-496, 1993

A/Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on i

A/Reference number: F45722; MID:93100833; PMID:7677958

A/Accession: F45722
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: nucleic acid
A/Residues: 1-120 <SIM>
A/Cross-references: UNIPARC:UPI0000176D4D

A:Note: sequence extracted from NCBI backbone (NCBI:P120594)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: glycoprotein
F:15-99/Domain: immunoglobulin homology <Imm>

Query Match	38.9%;	Score 496.5;	DB 2;	Length 120;
Best Local Similarity	78.3%;	Pred. No. 3.5e-26;		
Matches 94;	Conservative 11;	Mismatches 14;	Indels 1;	Gaps 1.

QY 2 QVQLQSGPELIERKASVLTSLCAASGYSFTGTMMNWKQSHKSLIEWTGLITTPNCASS 60

Db 1 EVQLQSGPELVKPKASMKISCAASGYSFTGTMMNWKQSHKSLIEWTGLININNGTS 60

QY 61 YNKRFGKALITLDKSSFTAMDISTSESDANVFCARGGIDGRGPPYWGQITTYVSS 120

Db 61 YNKRFGKALITLDKSSFTVTEHLSLTSSESDANVFCARGGRDALDSWGQISVTVSS 120

RESULT 15

Ig kappa chain V region (27.10.2) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 21-Jan-2000
C/Accession: B30562
R/Sikder, S.K.; Borden, P.; Grunezo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison, S.L.
J. Immunol. 142, 888-893, 1989
A/Title: Amino acid substitutions in V-H CDR2 change the idiotype but not the antigen-binding site
A/Reference number: A30562; MUID:89110066; PMID:2464031
A/Accession: B30562
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-107 <SIK>
A/Cross-references: UNIPARC:UPI00001767BA
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
I;16-89/Domain: immunoglobulin homology <IIM>

Query Match	38.9%	Score 496;	DB 2;	Length 107;
Best Local Similarity	90.5%;	Pred. No. 3.3e-26;		
Matches 95;	Conservative 2;	Mismatches 8;	Indels 0;	Gaps 0

QY 137 IELTOSPAIMASPGKMTMTCSASSSVYHMYQOKGTSPKRIYVTSKLAAGVGRF 196
Db 2 IVLQSPAIMASPGKMTMTCSASSSVYHMYQOKGTSPKRNVDTSKLAAGVTRF 61
QY 197 SSGSGSGSYLTSSVEARDPATYTCQOMSGPLTFPGAGTKLEIK 241
Db 62 SSGSGSGSYLTSSVEARDPATYTCQOMSSNPYFGAGTKLEIK 106

Search completed: April 3, 2006, 05:30:51
Job time : 23 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 3, 2006, 05:30:20 ; Search time 56 Seconds

(without alignments)
3036.291 Million cell updates/sec

Title: US-09-979-539-1

Perfect score: 1276
Sequence: 1 MOVOLQSGSPLEKPGASVK.....CQWNGYPLTFCAGTKLEIK 241

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: uniprot_05.80:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	792.5	62.1	243	2	Q7TQM2_MOUSE
2	783.5	61.4	244	2	Q65ZC8_HUMAN
3	771.5	60.5	487	2	Q65ZL2_9MURI
4	733.5	57.5	255	2	Q6KB03_MOUSE
5	726.5	56.9	241	2	Q921A6_MOUSE
6	718.5	56.3	240	2	Q652C9_HUMAN
7	645	50.5	248	2	Q652Q7_9MURI
8	628	49.2	218	2	Q925S1_MOUSE
9	543	47.6	170	2	Q925S2_MOUSE
10	514.5	40.3	470	2	Q7TQM1_MOUSE
11	502.5	39.4	472	2	Q6JUA7_MOUSE
12	497	38.9	483	2	Q4VAB6_MOUSE
13	496	38.9	112	2	Q8X1F0_MOUSE
14	496	38.9	235	2	Q58EV6_MOUSE
15	495.5	38.8	488	2	Q91WR1_MOUSE
16	492.5	38.6	118	1	HV51_MOUSE
17	491	38.5	107	1	KV6F_MOUSE
18	486	38.1	107	1	KV6I_MOUSE
19	486	38.1	117	2	Q9QXE9_MOUSE
20	485	38.0	107	1	KV6H_MOUSE
21	485	38.0	120	2	Q920E8_MOUSE
22	484	37.9	107	1	KV6G_MOUSE
23	483	37.8	117	2	Q9QXFO_MOUSE
24	482	37.8	134	2	Q8VYD0_MOUSE
25	481.5	37.7	481	2	Q8VCV5_MOUSE
26	480	37.6	107	1	KV6J_MOUSE
27	478	37.5	117	1	HV12_MOUSE
28	478	37.5	117	1	HV13_MOUSE
29	473	37.1	134	2	Q652R6_MOUSE
30	472.5	37.0	473	2	Q9DB14_MOUSE
31	472.5	37.0	477	2	Q58E56_MOUSE

32	469.5	36.8	458	2	Q5BJ22_RAT	Q5BJ22_rattus norv
33	468.5	36.7	485	2	Q58E61_MOUSE	Q58E61_mus musculu
34	468	36.7	112	2	Q8K1F2_MOUSE	Q8K1F2_mus musculu
35	467.5	36.6	468	2	Q569W9_MOUSE	Q569W9_mus musculu
36	467	36.6	465	2	Q6FUB2_MOUSE	Q6FUB2_mus musculu
37	466	36.5	123	2	Q8V1J1_MOUSE	Q8V1J1_mus musculu
38	462.5	36.2	598	2	Q568Y0_MOUSE	Q568Y0_rattus norv
39	462	36.2	136	1	HV15_MOUSE	P01759_mus musculu
40	459	36.0	481	2	Q91WT1_MOUSE	Q91WT1_mus musculu
41	457	35.8	112	2	Q8K1F3_MOUSE	Q8K1F3_mus musculu
42	457	35.8	114	2	Q8K1F1_MOUSE	Q8K1F1_mus musculu
43	453.5	35.5	482	2	Q8K172_MOUSE	Q8K172_mus musculu
44	453	35.5	142	2	Q924Q1_MOUSE	Q924Q1_mus musculu
45	453	35.5	237	2	Q569Y8_MOUSE	Q569Y8_mus musculu

ALIGNMENTS

RESULT 1	ID	Q7TQM2_MOUSE	PRELIMINARY;	PRT;	243 AA.
AC	Q7TQM2;				
DT	01-OCT-2003	(Tremblrel. 25, Created)			
DT	01-OCT-2003	(Tremblrel. 25, Last sequence update)			
DT	01-MAR-2004	(Tremblrel. 26, Last annotation update)			
DE	Scfv 6H8 protein (Fragment).				
GN	Name=SCFV 6H8;				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;				
OC	Muridae; Murinae; Mus.				
OX	NCBI_Taxid=10090;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE.				
RC	STRAIN=Balb/C;				
RX	MEDLINE=22853226; PubMed=12860977; DOI=10.1074/jbc.M306877200;				
RA	Peter J.C., Fifehah P., Billiald P., Wallukat G., Hoebeke J.;				
RT	"scfv single chain antibody variable fragment as inverse agonist for				
RT	the beta-2 adrenergic receptor.";				
RL	J. Biol. Chem. 278:36740-36747(2003).				
DR	EMBL; AJ574851; CAE00495.1; -; Genomic_DNA.				
DR	HSSP; P01751; 1A6W.				
DR	SMR; Q7TQM2; 1-236.				
DR	InterPro; IPR007110; IG-like.				
DR	InterPro; IPR003596; IG_V.				
DR	SMART; SM00406; IG_V.				
DR	PROSITE; PS50835; IG_LIKE; 2.				
DR	NON TER				
DR	SEQUENCE 243 AA; 25976 MW; BEFF642DCAF76 CRC64;				
Query Match	62.1%;	Score 792.5;	DB 2;	Length 243;	
Best Local Similarity	64.9%;	Pred. No. 1.3e-53;			
Matches 157;	Conservative 30;	Mismatches 48;	Indels 7;	Gaps 4;	
QY	2	QVOLIQQSGSPLEKPGASVKLSCKASGYSGFTYTMNVMVQSHGKSLWIGLITPYNGASSY	61		
DB	1	QVOLIQQSGSELVRPGASVKLSCKASGYFTITMNMVMVQSHGKSLWIGLITPYNGASSY	60		
QY	62	NOKRGRKTLTVNDKSSSTAYMDLSTSEDAVYFCAGRGYDGRFPDYWGQGTITTVSSG	121		
DB	61	DEKFNKILTVNDKSSSTAYMDLSTSEDAVYFCAGRGYDGRFPDYWGQGTITTVSSG	117		
QY	122	VGSGGGGGGGGGSDILTQSPALMSAPGKVTMTCSASSV--SYNMYOQKSGTSPKR	180		
DB	118	GGSGGGGGGGGGSDILTQSPALMSAPGKVTMTCSASSV--SYNMYOQKSGTSPKR	177		
QY	181	WIYDTSLKASVPGFSGSGSGSYLTSSVEAEDDATYTCQ--WSGYPLTPGAGTYLE	239		
DB	178	LISGATSLKASVPGFSGSGSGSYLTSSVEAEDDATYTCQ--WSGYPLTPGAGTYLE	235		
QY	240	IK 241			

DB 236 IK 237

RESULT 2
065ZL8 HUMAN PRELIMINARY; PRT; 244 AA.

ID 065ZC8 HUMAN PRELIMINARY; PRT; 244 AA.

AC 065ZC8;

DT 25-OCT-2004 (TREMBlrel. 28, Created)

DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)

DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)

DE Single-chain Fv (Fragment).

GN Name=scFv;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Carnivora; Homiidae;

OC Homo.

NCBI_TaxID=9606;

OK NCB1_TaxID=9606;

RN NUCLEOTIDE SEQUENCE.

RP MEDLINE=97362799; PubMed=9219263; DOI=10.1038/nbt0797-629;

RX Kontermann R.E., Wing M.G., Winter G.;

RT "Complement recruitment using bispecific diabodies.";

RL Nat. Biotechnol. 15:629-631(1997).

DR EMBL; Y13057; CAA73500.1; -; mRNA.

DR InterPro; IPR003599; I9.

DR InterPro; IPR007110; I9-like.

DR InterPro; IPR003596; I9_v.

DR SMART; SM00409; I9; 2.

DR SMART; SM00406; I9v; 2.

DR PROSITE; PS50835; I9_LIKE; 2.

FT NON_TER 1 244

FT NON_TER 1 244

SQ SEQUENCE 244 AA; 26127 MW; 4B1F17868338F2BF CRC64;

Query Match 61.4%; Score 783.5; DB 2; Length 244;
Best Local Similarity 61.3%; Pred. No. 6.6e-53;
Matches 149; Conservative 39; Mismatches 52; Indels 3; Gaps 2;

QY 2 QVQLQSGPELEKPGASVYLSCKASGYSTGYTMNWKVSHGKSLIEWIGLITPYNGASSY 61

DB 1 QVQLVQSGAEVKKPKPGSVKVSCKASGYTFSDFYMHVNRQAPCGLEMMQWIDPNNQDTFR 60

QY 62 NQKFRGKATLTVDKSSSTAYMDLSTSEDSAVYFCARGYDGR--GPDYWGQGTYYVS 119

DB 61 AAFPGQRTVTRDTSTSAAYMEVSRLRSDITAVYICAREGTSATYGMVQGTLYVVS 120

QY 120 SGGVSGGGGGGGGGSDIELTQSPALMSAPGKVTMTCSASSV-SYMHVYQOKSGTSP 178

DB 121 SGGGGGGGGGGGGGGSDIQWTQSPSTLSASIGDRVTITCRASBGIVHMLAWYQOKFGKAP 180

QY 179 KRWIYDTSLASGVPGRFSGSGSNYSLTISVEAEDDATYVCOQMSGYPLTFGAGTKL 238

DB 181 KFLIYVASSLASGAPFRFSGSGSDFTLTSLQPDPAIYCCQYSNYPILFGGGL 240

QY 239 EIK 241

DB 241 EIK 243

RESULT 3
065ZL2 9MURI PRELIMINARY; PRT; 487 AA.

ID 065ZL2 9MURI PRELIMINARY; PRT; 487 AA.

AC 065ZL2;

DT 25-OCT-2004 (TREMBlrel. 28, Created)

DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)

DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)

DE FV/M4.

GN Name=M4-IFN- ϵ tau;

OS Mus sp.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Muridae; Murinae; Mus.

NCBI_TaxID=10095;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=965272580; PubMed=8688499;

QY Y., Xiang J.;

RT "A genetically engineered single-gene-encoded anti-TAG72 chimeric antibody secreted from myeloma cells.";

RL Hum. Antibodies Hybridomas 6:161-166(1995).

DR EMBL; S82493; AAB37424.2; -; mRNA.

DR GO; GO:0003823; F:antigen binding; IEA.

DR InterPro; IPR003599; I9.

DR InterPro; IPR007110; I9-like.

DR InterPro; IPR003597; I9_c1.

DR InterPro; IPR003598; I9_c2.

DR InterPro; IPR003006; I9_MHC.

DR InterPro; IPR003596; I9_v.

DR Pfam; PF07654; C1-set; 2.

DR SMART; SM00409; I9; 3.

DR SMART; SM00407; I9c1; 2.

DR SMART; SM00408; I9c2; 2.

DR SMART; SM00406; I9v; 2.

DR PROSITE; PS50835; I9_LIKE; 4.

DR PROSITE; PS00290; I9_MHC; 1.

SQ SEQUENCE 487 AA; 53578 MW; C7BAB69F30555504 CRC64;

Query Match 60.5%; Score 771.5; DB 2; Length 487;
Best Local Similarity 63.5%; Pred. No. 1.3e-51;
Matches 153; Conservative 28; Mismatches 53; Indels 7; Gaps 3;

QY 2 QVQLQSGPELEKPGASVYLSCKASGYSTGYTMNWKVSHGKSLIEWIGLITPYNGASSY 61

DB 20 QVQLQSGDAELVKGASVYKISCKASGYTFDTHAHMAKQKPEQGLEWIGYSPGNDLIK 79

QY 62 NQKFRGKATLTVDKSSSTAYMDLSTSEDSAVYFCARGYDGRGPDYWGQGTYYVS 121

DB 80 NEKFRGKATLTVDKSSSTAYMDLSTSEDSAVYFCARGYDGRGPDYWGQGTYYVS 133

QY 122 VGGSGGGGGGGGGSDIELTQSPALMSAPGKVTMTCSASSV-SYMHVYQOKSGTSPKR 180

DB 134 GGGSGGGGGGGGGGGSDIQWTQSPSTLSASIGDRVTITCRASBGIVHMLAWYQOKFGKAP 193

QY 181 WIYDTSLASGVPGRFSGSGSNYSLTISVEAEDDATYVCOQMSGYPLTFGAGTKLEI 240

DB 194 LVYATNLADGVPSRFSGSGSGGTQSLKINLSQEDFSGYCCQHPWGTPTPTFGGTRLEI 253

QY 241 K 241

DB 254 K 254

RESULT 4
06KB05 MOUSE PRELIMINARY; PRT; 255 AA.

ID 06KB05 MOUSE PRELIMINARY; PRT; 255 AA.

AC 06KB05;

DT 05-JUL-2004 (TREMBlrel. 27, Created)

DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)

DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)

DE scFv B8E5 protein (Fragment).

GN Name=scFv B8E5;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Muridae; Murinae; Mus.

NCBI_TaxID=10090;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=Balb/c;

RA Peter J.C., Walikat G., Tugler J., Maurice D., Roegel J.C.,
Briand J.P., Hoebeke J.;

RT "Modulation of the M2 muscarinic acetylcholine receptor activity with monoclonal anti-M2 receptor antibody fragments.";

RL J. Biol. Chem. 279:55697-55706(2004).

DR EMBL; AJ746180; CAG34081.1; -; Other_DNA.

DR HSPF; P01837; IKCR.

DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003596; IG_v.
DR SMART: SM00409; IG; 2.
DR SMART: SM00406; IG; 2.
DR PROSITE: PS50835; IG_Like; 2.
FT NON TER 1 1
SQ SEQUENCE 255 AA; 27445 MW; B68BD38395DF713B CRC64;

Query Match 57.5%; Score 733.5; DB 2; Length 255;
Best Local Similarity 57.6%; Pred. No. 5.3e-49;
Matches 144; Conservative 35; Mismatches 60; Indels 11; Gaps 3;

QY 2 QVQLQSGPELEKPGASVYLSCKASGYSTGYTMNWKSHGSLKSLWIGLITPYNGASSY 61
DB 1 QVQLQSGPELEKPGASVYLSCKASGYSTGYTMNWKSHGSLKSLWIGLITPYNGASSY 60
QY 62 NQKFRGKATLVVDKSSSTAYMDLSTLSEDAVYFCARG---GYDRGPDYWGQGTITVY 118
DB 61 PDSVKGRFTISRDNKNTIYLQMSLSKSDTAMTYCARHINRYDG-AFDYWGQGTITLV 119
QY 119 SSGVGGSGGGSGGSDIELTQSPAIMSAPGEKVTMTCSASSV-----SYHWYQ 171
DB 120 SSGGGSGGGSGGGSDIYMAQSPSLSEVSAKEKIVMSCKSQSLNLRNOKNYLAWYQ 179
QY 172 QKSGSPKRWITDTSKLSGVPRFGSGSGNSYSLTISVBAEDATYCCQMSGYPLT 231
DB 180 QKGGSPKLLITYGASTRESGVPDRFTGSGSGTDFLTITSSVQAEADLAVYVCNDHSYPLT 239
QY 232 FGAGTKLEIK 241
DB 240 FGAGTKLEIK 249

RESULT 5
Q921A6 MOUSE PRELIMINARY; PRT; 241 AA.

AC Q921A6;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Anti-CEA 79 single chain Fv (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98170165; PubMed=9509426;
RA Chung J.H., Choi S.U., Kim H.U., Kim I.H., Choi I.H., Lee S.D.,
Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;
RT "Cloning and characterization of cDNAs encoding VH and VL of a
monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and
RT generation of a single-chain Fv molecule (scFv).";
RL Mol. Cells 7:816-819(1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=91341421; PubMed=1908510; DOI=10.1084/jem.174.3.613;
RA Stark S.B., Caton A.J.;
RT "Antibodies that are specific for a single amino acid interchange in a
RT protein epitope use structurally distinct variable regions.";
RL J. Exp. Med. 174:613-624(1991).

DR EMBL: U88067; AAB48044.1; -, mRNA.
DR PIR: S1965; S1965.
DR PIR: S1967; S1967.
DR PIR: S1968; S1968.
DR PIR: S26325; S26325.
DR HSSP: P01607; 1BWW.
DR EMBL: ENSMUSG00000021155; Mus musculus.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003596; IG_v.
DR SMART: SM00406; IG; 2.

DR PROSITE: PS50835; IG_Like; 2.
FT NON TER 1 1
FT NON TER 241 241
SQ SEQUENCE 241 AA; 26086 MW; 0276887248B9C771 CRC64;

Query Match 56.9%; Score 726.5; DB 2; Length 241;
Best Local Similarity 58.8%; Pred. No. 1.8e-48;
Matches 144; Conservative 34; Mismatches 56; Indels 11; Gaps 5;

QY 2 QVQLQSGPELEKPGASVYLSCKASGYSTGYTMNWKSHGSLKSLWIGLITPYNGASSY 61
DB 1 QVQLQSGPELEKPGASVYLSCKASGYSTGYTMNWKSHGSLKSLWIGLITPYNGASSY 60
QY 62 NQKFRGKATLVVDKSSSTAYMDLSTLSEDAVYFCARGVDYDRGPDYWGQGTITVYSSG 121
DB 61 ADFFGRAPFSLTETASSTAYLIQINLKNEDTATYFCARDL-LRYFDYWGQGTITVYSSG 119
QY 122 VGGSGGGSGGGSGSDIELTQSPAIMSAPGEKVTMTCSASSV-SYHWYQKSGTSPK 180
DB 120 GGGSGGGSGGGSGSDIELTQSPSLASLGGKVTITCKASQDINKYIANYQHKPKGRPS 179
QY 181 ----WYDTSKLSGVPRFGSGSGNSYSLTISVBAEDATYCCQMSGYPLTFGAGT 236
DB 180 AHTLHIT----IQGIPERFGSGSGGRDYSFISNLFREDIATYCLHYDNLH-TFGGCT 234
QY 237 KLEIK 241
DB 235 KLEIK 239

RESULT 6
Q65ZC9 HUMAN PRELIMINARY; PRT; 240 AA.

AC Q65ZC9;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Single-chain Fv (Fragment).
GN Name=scFv;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C1G/7;
RX MEDLINE=97362799; PubMed=9219263; DOI=10.1038/nbt0797-629;
RA Kontermann R.B., Wing M.G., Winter G.;
RT "Complement recruitment using bispecific diabodies.";
RL Nat. Biotechnol. 15:629-631(1997).
DR EMBL: Y13056; CAA73499.1; -, mRNA.
DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG-Like.
DR InterPro: IPR003596; IG_v.
DR SMART: SM00409; IG; 2.
DR SMART: SM00406; IG; 2.
DR PROSITE: PS50835; IG_Like; 2.
FT NON TER 1 1
FT NON TER 240 240
SQ SEQUENCE 240 AA; 25569 MW; FDCFPD3645F64B373 CRC64;

Query Match 56.3%; Score 718.5; DB 2; Length 240;
Best Local Similarity 57.4%; Pred. No. 7.3e-48;
Matches 139; Conservative 43; Mismatches 55; Indels 5; Gaps 4;

QY 2 QVQLQSGPELEKPGASVYLSCKASGYSTGYTMNWKSHGSLKSLWIGLITPYNGASS- 60
DB 1 QVQLVGGGGIVQGGSLRLSCASGFTFSYGMHWYQAPGKGLKMWAVIS-YDGSNRY 59
QY 61 YNQKFRGKATLVVDKSSSTAYMDLSTLSEDAVYFCARGVDYDRGPDYWGQGTITVYSS 120
DB 60 YADSVKGRFTISRDNKNTIYLQMSLSKSDTAMTYCARHINRYDG-AFDYWGQGTITLVYSS 117

QY	121	GVGSGGGGGSGCGSDIELTOSPALMSASPGKMTVMTCASSV--SYHMFOOKSGTSRK	179
Db	118	GGGGGGGGSGGGSGSDIQMTOOSPSTLSIASIGRVITTCASBGITYMLMWIYOOKPEKAIX	177
QY	180	RMIYDYSKLASGVPRFSGSGSGNSYSLTISSEVEADDAATYYCQOMSGYPILTFGAGTKLE	239
Db	178	LIIYASSLASAPRPFSGSGSGTDPTLTISSLQPDPATYYCCQYSNIPPLTFGGGTKLE	237
QY	240	IK 241	
Db	238	IK 239	

	RESULT	7	
ID	065Z07_9MURI	PRT;	248 AA.
AC	065Z07_9MURI PRELIMINARY;		
DT	065Z07_9MURI PRELIMINARY;		
DT	25-OCT-2004 (TREMBlrel. 28, Created)		
DT	25-OCT-2004 (TREMBlrel. 28, Last sequence update)		
DT	25-OCT-2004 (TREMBlrel. 28, Last annotation update)		
DE	B3 (Fv)-PE40 (Fragment).		
GN	Name=B3 (Fv)-PE40;		
OS	Mus sp.		
OC	Eumariota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
CC	Bivalvia; Euthera; Euarchoctoglossi; Glires; Rodentia; Sciurognathi;		
OC	Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10095;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
EX	MEBLINE=972020904; PubMed=1924123;		
RA	Brinkmann U., Pal L.H., FitzGerald D.J., Willingham I.,		
RT	"B3(Fv)-PE38DEL, a single-chain immunotoxin that causes complete		
RL	regression of a human carcinoma in mice." ;		
RT	Proc. Natl. Acad. Sci. U.S.A. 88:8616-8620(1991) .		
DR	EMBL; S57990; AAB19971.2; -; mRNA.		
DR	SMR; 065Z07; 4-247.		
DR	InterPro; IPR003599; IG_1like.		
DR	InterPro; IPR007110; IG_1like.		
DR	InterPro; IPR003596; IG_v.		
DR	SMART; SMO0409; IG; 2.		
DR	SMART; SMO0406; IG; 2.		
DR	PROSITE; PS50835; IG LIKE; 2.		
FT	NON_TER	248	
SO	SEQUENCE	248 AA; 26634 MW; 7A3759BA3E570950 CRC64;	

	Query Match	50.5%;	Score 645;	DB 2;	Length 248;
	Best Local Similarity	51.0%;	Pred. No. 3_9e-42;		
	Matches	126;	Conservative	41;	Mismatches 74; Indels 6; Gaps 1
QY		1	MOVOLQGSPLEIEKFGASVYKLSCCKASGVSFTGTVMWVKQSCKSLSELTGITLPINGASS	60	
Db		1	MDVKLVESGGGLVQPGSILKLSCATSGFFPSFYIYWVAWQTBEKRLIEWAYLISNDSSAA	60	
QY		61	YNQKEFGKATLLTVDDSSSTAYAMDLLSTLESBDAVFCARGYGDRGFDMVGQTTVTVAS	120	
Db		61	YSDTYKGRFTISRDNARNTLTYLQMSRSLKSEDPTAIYSCARGLAMGAFAWMGQTLVTVAS	120	
QY		121	GVGSGGGGGSGGGSDIELTOSPALMSAPGEKVMTGCASSV-----SYMHWYQQKS	174	
Db		121	GGGSGGGGGSGGGSDVLMTOSPLPVSLGDPAASICSSQTIYHSNGNTLLEYTLQCP	180	
QY		175	GTSPPKMIYDTSKLASGVPGAREFSGSGSGNSYSILLTISVEAEDDATYYYCOOMSGPYLTFGA	234	
Db		181	GQSPKLLIIKYVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLIGYYVCFQGSHPVPTFGS	240	
QY		235	GTKLEIK 241		
Db		241	GTKLEIK 247		

RESULT 8
Q925S1_MOUSE

ID	G925S1	MOUSE PRELIMINARY;	PRT;	218 AA.
AC	G925S1;			
DT	01-DEC-2001	(TREMBLrel. 19, Created)		
DT	01-DEC-2001	(TREMBLrel. 19, Last sequence update)		
DT	01-OCT-2003	(TREMBLrel. 25, Last annotation update)		
DE	MRP5 (Fragment).			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;			
OC	Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RC	NUCLEOTIDE SEQUENCE.			
RP	STRAIN=BALB/c;			
RX	PubMed=11819679;			
RA	Cui D.X., Zeng G.Y., Wang F., Xu J.R., Ren D.Q., Guo Y.H., Tian F.R.,			
RA	Yan X.J., Hou Y., Su C.Z.;			
RT	"Mechanism of exogenous nucleic acids and their precursors improving			
RT	the repair of intestinal epithelial cells after gamma-irradiation in mice."			
RL	World J. Gastroenterol. 6:709-717(2000).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE.			
RC	STRAIN=BALB/c;			
RA	Cui D., Zeng G., Yan X., Li X., Su C.;			
RT	"Cloning of mouse genes related to repairing of intestinal epithelium			
RT	of the irradiated mice by treatment with the intestinal RNA of mice of			
RT	the same strain."			
RT	Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).			
DR	EMBL; AP240168; AAK43733.1; -; mRNA.			
DR	HSSP; P01665; IONZ.			
DR	ENSEMBL; ENSMUSG0000058040; Mus musculus.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003596; Ig_v.			
DR	SMART; SM00406; IGV; 1.			
DR	PROSITE; PSS0835; IG_LIKE; 1.			
FT	NON TER			
FT	218			
FT	218			
SEQUENCE	218 AA; 23013 MW; 527B4FA8F7982817 CRC64;			

Query Match	Similarity	49.2%	Score 628	DB 2	Length 218
Best Local	Similarity	55.8%	Pred. No. 7e+11		
Matches	121	Conservative	35	Mismatches	55
				Indels	6
				Gaps	2

QY	2	QVQLQDSGP	ELKPKGASVKLSCKASGYSTFTYTNMVKSHGSKLEMIIGLTTPNGASSY	61
DB	3	QVTLQDSGP <td>ELKPKRGETVRIISCKASGYTFTTAGKQWVQKMPGSKLKKMIWINTHSGVPKY</td> <td>62</td>	ELKPKRGETVRIISCKASGYTFTTAGKQWVQKMPGSKLKKMIWINTHSGVPKY	62
QY	62	NQKRGRKATLTVDKSSSTAYMDLSLTSSEDAVYFCARGIDGKGFDTYWGQGT	121	121
DB	63	AEEFKGRFAFSLERSTASTAYLQISLNKNEIDPATYFCMRWDYD-G	121	121
QY	122	VGGSGGGSGGGSGGSDILTLOSPATMSAPGKVMTCSSASSY-----SYWHWYQOKSGT	176	176
DB	122	GGSGGGSGGGSGGSDIVLTQSPALVALSLGPRATISCRASSVDNIGISFNNWFOQKPGQ	181	181
QY	177	SPKRWYDTSKLAGSVGRFSGSGSGNVSYSLTISSE	213	213
DB	182	PPKLLITTAASKGSGVPAAGLLASSGDTFSLNITPME	218	218

RESULT 9	0925S2 MOUSE	Q925S2_MOUSE PRELIMINARY;	PRT;	170 AA.
AC	Q925S2;			
DT	01-DEC-2001 (TREMBlrel. 19, Created)			
DT	01-DEC-2001 (TREMBlrel. 19, Last sequence update)			
DT	01-OCT-2003 (TREMBlrel. 25, Last annotation update)			
DE	MRP4.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;			
OC	Muroidea; Muridae; Murinae; Mus.			
CC	NCBI_TaxID=10090;			
RN	[1]			

RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=BALB/c;
 RC PubMed=11819679;
 RA Cui D.X., Zeng G.Y., Wang F., Xu J.R., Ren D.Q., Guo Y.H., Tian F.R.,
 RA Yan X.Y., Hou Y., Su C.Z.;
 RA "Mechanism of exogenous nucleic acids and their precursors improving
 RT the repair of intestinal epithelium after gamma-irradiation in mice";
 RL World J. Gastroenterol. 6:709-717(2000).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=BALB/c;
 RA Cui D., Zeng G., Yan X., Li X., Su C.;
 RT "Cloning of mouse genes related to repairing of intestinal epithelium
 RT of the irradiated mice by treatment with the intestinal RNA of mice of
 RT the same strain";
 RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
 DR EMBL; AF240167; AK43732.1; -, mRNA.
 DR HSSP; P01751; 1A6W.
 DR SMR; Q92582; 3-124.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR SMART; SM00406; IGV, 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin domain.
 SQ SEQUENCE 170 AA; 17978 MW; 5042823C6C10F38 CRC64;
 Query Match 42.6%; Score 543; DB 2; Length 170;
 Best Local Similarity 66.4%; Pred. No. 2.1e-34;
 Matches 101; Conservative 23; Mismatches 16; Indels 12; Gaps 2;
 QY 2 OVQLQSSPELEKPGASVYLSCKASGYSTGYTMNVMVQSHGKSLFWIGLITPYNGASGY 61
 DB 3 QVQLQSSPEVVRPVSYSKISCKSGSYTTDYSMHKNHMQSLFWIGLITPYNGVNTY 62
 QY 62 NQKFRGKATLVNKKSSSTAYMDLSTLSEDSAVYFCARGGYDGR--GPDYWGQGTIVVS 119
 DB 63 NQKFRGKATLVNKKSSSTAYMDLSTLSEDSAVYFCARGGYDGR--GPDYWGQGTIVVS 122
 QY 120 SGVGGSGGGSGGGSGGSDIELTQSPALMASPG 151
 DB 123 SGGSGSGGGSGGGSGGSE-----SSSPG 144
 RESULT 10
 Q7TMK1_MOUSE
 ID Q7TMK1_MOUSE PRELIMINARY; PRT; 470 AA.
 AC Q7TMK1;
 DT 01-OCT-2003 (TREMBlrel. 25, Created)
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Hypothetical protein A1324046.
 GN Name=A1324046;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OK NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J;
 RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.
 RC Expression driven by an MMTV-LTR enhancer.;
 RC MEDLINE=22388527; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold R.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stadelton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzyzanski M.I., Skalski U., Smallus D.E.,
 RA Schercher A., Schin J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J;
 RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.
 RC Expression driven by an MMTV-LTR enhancer.;
 RA Strausberg R.;
 RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC055910; AAH5910.1; -, mRNA.
 DR HSSP; P01865; 1XB5.
 DR GO; GO:0003823; P:antigen binding; IEA.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF07654; CI-setc; 3.
 DR SMART; SM00406; IGV, 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
 KW Hypothetical protein; Immunoglobulin domain.
 SQ SEQUENCE 470 AA; 51728 MW; 6D90E4DF896B090 CRC64;
 Query Match 40.3%; Score 514.5; DB 2; Length 470;
 Best Local Similarity 52.1%; Pred. No. 1.1e-31;
 Matches 122; Conservative 19; Mismatches 46; Indels 47; Gaps 8;
 QY 2 OVQLQSSPELEKPGASVYLSCKASGYSTGYTMNVMVQSHGKSLFWIGLITPYNGASGY 61
 DB 20 EVQLQSSPELVKPGASVKISKSGSYFTGYTMNVMVQSHGKSLFWIGLITPYNGSDPSY 79
 QY 62 NQKFRGKATLVNKKSSSTAYMDLSTLSEDSAVYFCARGGYDGR--GPDYWGQGTIVVS 119
 DB 80 NQKFRGKATLVNKKSSSTAYMDLSTLSEDSAVYFCARGGYDGR--GPDYWGQGTIVVS 139
 QY 120 SGVGGSGGGSGGGSGGSDIELTQSPALMASP-----GKTYTMCSSASSSYVMHYQOK 173
 DB 140 SAT-----TPASVYPVLYGCGDPTSGSVTLGCLV----- 169

RESULT 11
 O6PJA7_MOUSE
 ID O6PJA7_MOUSE PRELIMINARY; PRT; 472 AA.
 AC O6PJA7;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Hypothetical protein.
 GN Name=Igh-1a;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OK NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J;
 RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.
 RC Expression driven by an MMTV-LTR enhancer.;
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold R.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gamaralle P.H.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Czech II;
 RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.
 RC Expression driven by an MMTV-LTR enhancer.;
 RL Strausberg R.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC018535; AAH18535.1; -; mRNA.
 DR HSSP; P01865; 1KB5.
 DR MGI; MGI:96443; 1gh-1a.
 DR GO; GO:0003823; F-antigen binding; IEA.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PR07654; C1-set; 3.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGc1; 3.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS00835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 472 AA; 52299 MW; 165169C23D55D4AB CRC64;

Query Match 39.4%; Score 502.5; DB 2; Length 472;
 Best Local Similarity 46.1%; Pred. No. 9.8e-31;
 Matches 118; Conservative 26; Mismatches 59; Indels 53; Gaps 9;

QY 2 QVQLQSGPELEKPGASVYLSCCKASGYSTGYTMNWKSHGKSLIEWIGLITPYNGASSY 61
 DB 20 EVQLQSGPELVLTGASVSKSCASGYTSDYTMHWKSHGKSLIEWIGITYPNNGNGY 79
 QY 62 NQKFRGKATLVYDKSSSTAYMDLSTSEDAVYFCARG----GYDGRGPDYWGQGTIV 116
 DB 80 NQKFRGKATLVYDKSSSTAYMDLSTSEDAVYFCARG----GYDGRGPDYWGQGTIV 138
 QY 117 TVSSGVGGSGGGGGSDIELTQSPALMASP-----GEKVTMTCSASSSVSYMYWY 170
 DB 139 TVSSA-----KTAPSVYPLAPVCGDTTGSVTLGCLVK---GYF--- 175
 QY 171 QOKSGSPKRMVDTYDKSLASGVPRGSPSGSGNSYSLTSSVAEDDAITYYCOQWGGYPL 230
 DB 176 -----DEPYTLTWNSSLSISGV-HTFPAVLQSDLYTLSSS-----VTVTSSTWSSGI 222
 QY 231 TF-----GAGTKLEIK 241
 DB 223 TCNVAPHPASTKYDKK 238

RESULT 12
 QVAB6_MOUSE PRELIMINARY; PRT; 483 AA.
 AC QVAB6;

DT 13-SEP-2005 (TREMBlrel. 31, Created)
 DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OK NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FVB/N; TISSUE=Colon;
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gamaralle P.H.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FVB/N; TISSUE=Colon;
 RG NIH MGC Project;
 RL Submitted (May-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC096462; AAH96462.1; -; mRNA.
 KW Hypothetical protein.
 SQ SEQUENCE 483 AA; 52436 MW; 368E7BEE6BDE9EF CRC64;

Query Match 38.9%; Score 497; DB 2; Length 483;
 Best Local Similarity 48.5%; Pred. No. 2.7e-30;
 Matches 114; Conservative 25; Mismatches 50; Indels 46; Gaps 7;

QY 2 QVQLQSGPELEKPGASVYLSCCKASGYSTGYTMNWKSHGKSLIEWIGLITPYNGASSY 61
 DB 20 EQLHSGPELVKPGTSYKMSCKASGYTFYTMHWKSHGKSLIEWIGITYPNNGNGY 79
 QY 62 NQKFRGKATLVYDKSSSTAYMDLSTSEDAVYFCARGVDGKGFDPYWGQGTIVTVSSG 121
 DB 80 NQKFRGKATLVYDKSSSTAYMDLSTSEDAVYFCARGVDGKGFDPYWGQGTIVTVSSG 138
 QY 122 VGSAGGGSGGGGGSDIELTQSPALMASP-----SASPEKVTMTCSASSSVSYMYWYQOKSGT 176
 DB 139 -----EPAREPTIYPLFPALASG--GRYTWSS-----QLTLPFAVECEGSGSVK 174
 QY 177 SPKRN-----LYDTSKLASGVPRGSPSGSGNSYSLTSSVAEDDAITYYCOQWGGYPL 222
 DB 175 MMTVTKSGSKDITTYNFPALASG--GRYTWSS-----QLTLPFAVECEGSGSVK 222

RESULT 13
 O8K1F0_MOUSE PRELIMINARY; PRT; 112 AA.
 AC O8K1F0;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Anti-VIPase light chain variable region (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
RN NCBI_TaxId=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BLB/C; TISSUE=Hyperimmunized spleen;
RA Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;
RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Colon;
RA Baccala R., Quang T.V., Gilbert M., Ternynck T., Avrameas S.;
RT "Two murine natural polypeptide autoantibodies are encoded by
RT nonmutated germ-line genes."; 86:4624-4628 (1989).
RL Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628 (1989).
DR EMBL; AF516285; AAM64203.1; -, Genomic_DNA.
DR PIR; A33933; A33933.
DR PIR; PC4405; PC4405.
DR HSSP; P01837; IOR0.
DR SMR; Q8K1F0; 3-112.
DR Ensemble; ENSMUSG0000062047; Mus musculus.
DR InterPro; IPR007110; Ig_V.
DR InterPro; IPR003596; Ig_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 112
SQ SEQUENCE 112 AA; 11901 MW; F6644663201A239 CRC64;
Query Match 38.9%; Score 496; DB 2; Length 112;
Best Local Similarity 92.2%; Pred. No. 5.7e-31;
Matches 95; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 139 LTQSPAIMSASPEKVTMTCSASSSVSYMHVYQKSGTSPKRWIYDTSKLASGVPRFSG 198
DB 4 LTQSPAIMSASPEKVTMTCSASSSVSYMHVYQKSGTSPKRWIYDTSKLASGVPRFSG 63
QY 199 SGGSGNSYSLTISVEAEDATYYCCQMSGVPLTFGAGTKLEIK 241
DB 64 SGGSGNSYSLTISVEAEDATYYCCQMSGVPLTFGAGTKLEIK 106
RESULT 14
Q58EV6 MOUSE PRELIMINARY; PRT; 235 AA.
ID Q58EV6; AC 058EV6;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Igh-C protein.
GN Name=Igh-C;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., McQuellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bobak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Colon;
RG NIH MGC Project;
RL Submitted (Mar-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC091738; AA91738.1; -, mRNA.
DR SMR; Q58EV6; 23-235.
DR GO; GO:0005823; Protein binding; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF07654; C1-set; I.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
DR PROSITE; PSS0290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 235 AA; 25719 MW; BE4E4ABDD2578252 CRC64;
Query Match 38.9%; Score 496; DB 2; Length 235;
Best Local Similarity 89.5%; Pred. No. 1.4e-30;
Matches 94; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
QY 137 IELTSPAIMSASPEKVTMTCSASSSVSYMHVYQKSGTSPKRWIYDTSKLASGVPRF 196
DB 24 IELTSPAIMSASPEKVTMTCSASSSVSYMHVYQKSGTSPKRWIYDTSKLASGVPRF 83
QY 197 SGGSGNSYSLTISVEAEDATYYCCQMSGVPLTFGAGTKLEIK 241
DB 84 SGGSGNSYSLTISVEAEDATYYCCQMSGVPLTFGAGTKLEIK 128
RESULT 15
Q91WR1 MOUSE PRELIMINARY; PRT; 488 AA.
ID Q91WR1; AC Q91WR1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Igh-VJ558 protein.
GN Name=Igh-VJ558;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., McQuellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bobak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield J.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Maita M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=FVB/N; TISSUE=Kidney;

RA Strausberg R.;

RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC013539; AAH13539.1; -; mRNA.

DR HSSP; P01751; 1A6W

DR Ensemble; ENSMUSG00000021155; Mus musculus.

DR MGI; MGI:96486; Igh-VJ558.

DR GO; GO:0003823; F:antigen binding; IEA.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig cl.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_V.

DR Pfam; PF07654; Cl-sec; 2.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG LIKE; 4.

DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.

KW Immunoglobulin domain.

SQ SEQUENCE 488 AA; 52965 MW; F12068460B400B9D CRC64;

Query Match 38.8%; Score 495.5; DB 2; Length 488;

Best Local Similarity 49.6%; Pred. No. 3.6e-30;

Matches 120; Conservative 20; Mismatches 47; Indels 55; Gaps 10;

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QY      2 QVQLQSGPELEKPKASVYLSCKASGYSTGYTMNWVKOSHGKSLFWIGLITPYNGASY 61
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Db      20 EVQLQSGPELVKPGASVTLSCKASGYTTIDYYVMWVKOSHGKSLFWIGDINPYNGTSY 79
QY      62 NQKFRKATLTVDKSSSTAYMDLSTLSDSAVYFCARG-----GYDGRGFDYWGQGT 114
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      80 NQKFRKATLTVDKSSSIAYMDLSTLSDSAVYFCARGPVYYSYFSD-RG-DYWGQGT 137
QY      115 TVTVSSGVGGSGGGSGGSDIELTQSPALM-----SASPEKVTMTCSASSSVYMW 169
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      138 LVTVSA-----EPAREPTIYPLTFPPQALSDPVIIGC-----LIHD 173
QY      170 YQKSGTSPKRW-----IYDTSKLASGVGPRFSGSGSGNSYSLTISVYAEADATY 220
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      174 Y-FPSCGMVMTWKGSGKDIYTVNFPALASG--GRYTWSS-----QLTLPAVECPGEGSV 225
QY      221 YC 222
      ||
Db      226 KC 227

```

Search completed: April 3, 2006, 05:31:28

Job time : 58 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 3, 2006, 05:29:59 ; Search time 323 Seconds

(without alignments)
327.834 Million cell updates/sec

Title: US-09-979-539-1

Perfect score: 1276
Sequence: 1 MQVQLQGSPELEKPGASVK.....CQMSGYPLTFGATKLEIK 241

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq.21.*

1: geneeqp1980s:*
2: geneeqp1990s:*
3: geneeqp2000s:*
4: geneeqp2001s:*
5: geneeqp2002s:*
6: geneeqp2003as:*
7: geneeqp2003bs:*
8: geneeqp2004s:*
9: geneeqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1276	100.0	241	2	ABR76197 Anti-meso
2	1276	100.0	241	4	ABR50019 Antimesot
3	1025.5	80.4	242	6	ABR62132 Single ch
4	1025.5	80.4	242	8	ADT91209 Single ch
5	1010.5	79.2	239	4	ABR47111 scFv 508P
6	1010.5	79.2	239	6	AAO16066 Human neu
7	1010.5	79.2	239	8	ADJ88113 Human bet
8	1004	78.7	494	9	ADV66089 Anti-CD3-
9	1004	78.7	500	9	ADV66137 Anti-CD3-
10	1004	78.7	500	9	ADV66095 Anti-CD3-
11	1004	78.7	500	9	ADV66097 Anti-CD3-
12	1004	78.7	503	9	ADV66131 Anti-CD3-
13	1004	78.7	503	9	ADV66093 Anti-CD3-
14	1004	78.7	503	9	ADV66091 Anti-CD3-
15	1004	78.7	503	9	ADV14540 Bispecifi
16	1004	78.7	503	9	AEA52450 Human CD3
17	1004	78.7	504	9	ADV14536 Bispecifi
18	1004	78.7	504	9	AEA52449 Human CD3
19	1003	78.6	261	8	ADT91213 Single ch
20	1002.5	78.6	498	8	ADW38798 Control s
21	998.5	78.3	239	7	ADC79232 Anti-CA12
22	997.5	78.0	242	2	AAR79872 Anti-EGFR
23	995	77.8	244	2	AAR79867 Anti-EGFR
24	993	77.8	244	2	AAR79867 Anti-EGFR

25	989.5	77.5	242	6	ABR62131	ABR62131 Single ch
26	989.5	77.5	242	8	ADT91207	ADT91207 Single ch
27	987	77.4	242	2	AAR79870	AAR79870 Anti-EGFR
28	985	77.2	244	2	AAR79873	AAR79873 Anti-EGFR
29	982.5	77.0	297	2	AAV05363	AAV05363 HBV spec
30	981.5	76.9	599	2	AAW37132	AAW37132 Anti-Tac
31	981.5	76.9	599	3	AAV87477	AAV87477 Anti-Tac
32	979.5	76.8	309	4	ABR70841	ABR70841 SNV-env 1
33	979	76.7	244	2	AAR79868	AAR79868 Anti-EGFR
34	977	76.6	242	2	AAR79871	AAR79871 Anti-EGFR
35	976.5	76.5	239	3	ABR12563	ABR12563 Anti-TAC
36	976.5	76.5	239	4	ABR36826	ABR36826 Anti-TAC
37	976.5	76.5	599	2	AAW95462	AAW95462 Anti-Tac
38	972.5	76.2	330	4	ABR70842	ABR70842 SNV-env 1
39	972	76.2	246	2	AAR79869	AAR79869 Anti-EGFR
40	967.5	75.8	492	8	ADQ91082	ADQ91082 Antibody
41	967.5	75.8	492	8	ADQ91098	ADQ91098 Antibody
42	967.5	75.8	492	8	ADQ91102	ADQ91102 Antibody
43	967.5	75.8	497	9	ADV66125	ADV66125 Anti-CD3-
44	967.5	75.8	503	9	ADV66087	ADV66087 Anti-CD3-
45	967.5	75.8	503	9	ADV66135	ADV66135 Anti-CD3-

ALIGNMENTS

RESULT 1	
ABR76197	ABR76197 standard; protein; 241 AA.
ID	ABR76197
XX	ABR76197;
AC	05-AUG-2002 (first entry)
XX	Anti-mesothelin scFv SS.
DT	Anti-mesothelin scFv SS.
XX	
DB	Mesothelin; antibody; scFv; mouse; mesothelioma; ovarian cancer;
XX	stomach cancer; squamous cell cancer; antitumour; therapy; diagnosis;
KW	immunotoxin.
KW	
XX	
OS	Mus sp.
XX	
PH	Key
FT	Region
FT	Location/Qualifiers
FT	1..31
FT	/note= "heavy chain framework region 1"
FT	32..36
FT	/note= "heavy chain complementarity determining region 1"
FT	37..50
FT	/note= "heavy chain framework region 2"
FT	51..67
FT	/note= "heavy chain complementarity determining region 2"
FT	68..99
FT	/note= "heavy chain framework region 3"
FT	100..109
FT	/note= "heavy chain complementarity determining region 3"
FT	110..120
FT	/note= "heavy chain framework region 4"
FT	121..135
FT	/note= "linker"
FT	136..158
FT	/note= "light chain framework region 1"
FT	159..168
FT	/note= "light chain complementarity determining region 1"
FT	169..183
FT	/note= "light chain framework region 2"
FT	184..190
FT	/note= "light chain complementarity determining region 2"
FT	191..222
FT	/note= "light chain framework region 3"
FT	223..231
FT	/note= "light chain complementarity determining region 3"
FT	232..241
FT	/note= "light chain framework region 4"

XX WO9928471-A2.
XX 10-JUN-1999.
XX 25-NOV-1998; 98WO-US025270.
XX 01-DEC-1997; 97US-0067175P.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX Pastan IH, Chowdhury PS;
XX WPI; 1999-371123/31.
XX DR N-PSDB; ABL57231.
XX New anti-mesothelin antibodies.
XX Claim 2; Fig 1; 63pp; English.
XX
XX The present sequence is the protein sequence of anti-mesothelin scFv antibody SS. This single-chain antibody was produced by immunising a mouse with cDNA encoding mesothelin, creating a phage library from mRNA isolated from the spleen of the immunised animal, and enrichment of anti-mesothelin phage over 3 rounds of panning. scFv SS is composed of a heavy chain variable region (VH) joined to a light chain variable region (VL) via a peptide linker. According to Kabat's classification, the VH belongs to sub-group IIA and family V and the VL belongs to sub-group VI and family XI. A claimed anti-mesothelin antibody binds recombinant mesothelin with a dissociation constant of less than 3×10^{-8} M and specifically binds to cells expressing mesothelin on their cell surface. The antibody comprises SS scFv, the VH and VL region of SS scFv or the complementarity determining regions of SS scFv. It is preferably conjugated to a therapeutic agent, particularly Pseudomonas exotoxin or its cytotoxic fragment. The resulting immunconjugate is used in a claimed method for inhibiting the growth of a malignant cell that expresses mesothelin on its cell surface, especially in mesothelioma, ovarian cancer, stomach cancer or squamous cell cancer. The antibody can also be used to detect mesothelin in a biological sample
SQ Sequence 241 AA;

Query Match 100.0%; Score 1276; DB 2; Length 241;

Best Local Similarity 100.0%; Pred. No. 1.8e-77;

Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 MOVVLQSGPELEKPGASVYKLSCKASGYSPFTGYTMWVKQSHGKSLIEWIGLITPPYNGASS 60
DB 1 MOVVLQSGPELEKPGASVYKLSCKASGYSPFTGYTMWVKQSHGKSLIEWIGLITPPYNGASS 60
QY 61 YNOKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGRGPDYWGQGTIVTVSS 120
DB 61 YNOKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGRGPDYWGQGTIVTVSS 120
QY 121 GVGSGGGGGSGGGSIDILTQSPAIMSASPGKVTMTCSASSSVSYMHMYOQKSGTSPKR 180
DB 121 GVGSGGGGGSGGGSIDILTQSPAIMSASPGKVTMTCSASSSVSYMHMYOQKSGTSPKR 180
QY 181 WIYDTSKLASGVPRFSGSGGNSYSLTISVEAEDDATYTCQOMSGYPLTFGAGTKLEI 240
DB 181 WIYDTSKLASGVPRFSGSGGNSYSLTISVEAEDDATYTCQOMSGYPLTFGAGTKLEI 240
QY 241 K 241
DB 241 K 241
```

RESULT 2
AAB50019
ID AAB50019 standard; protein; 241 AA.
XX
AC AAB50019;
XX

DT 14-MAR-2001 (first entry)
XX Antimesothelin antibody SS single-chain Fv protein.
DE Mesothelin; SS antibody; single-chain Fv; scFv; cytostatic;
XX cancer therapy; ovarian cancer; mesothelioma.
XX Unidentified.
XX WO200073346-A1.
XX 07-DEC-2000.
XX 26-MAY-2000; 2000WO-US014829.
XX 27-MAY-1999; 99US-0160071P.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX Pastan I, Chowdhury PS;
XX WPI; 2001-061517/07.
XX
XX Novel polypeptides comprising mutated antimesothelin antibody heavy or light chain variable region, having greater binding affinity for the antigen, useful as diagnostic and therapeutic agents for ovarian cancers.
XX Disclosure; Fig 1; 70pp; English.

The present sequence is antimesothelin antibody SS single chain Fv protein. This sequence was used to generate mutant antibody heavy or light chain variable regions, which have 5 times higher binding affinity for mesothelin antigen than the parental antibody (the present sequence). The mutant proteins of the present invention have substitution(s) in the complementarity determining region (CDR). Malignant cells express mesothelin on their surfaces, and so the mutant proteins of the present invention can be used to target immunotoxin to cells expressing mesothelin on their surface i.e. malignant cells. The mutant proteins of the present invention can therefore be used to treat ovarian cancers, mesotheliomas, and several other types of human cancers in which the cells bear the mesothelin antigen

SQ Sequence 241 AA;

Query Match 100.0%; Score 1276; DB 4; Length 241;

Best Local Similarity 100.0%; Pred. No. 1.8e-77;

Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 MOVVLQSGPELEKPGASVYKLSCKASGYSPFTGYTMWVKQSHGKSLIEWIGLITPPYNGASS 60
DB 1 MOVVLQSGPELEKPGASVYKLSCKASGYSPFTGYTMWVKQSHGKSLIEWIGLITPPYNGASS 60
QY 61 YNOKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGRGPDYWGQGTIVTVSS 120
DB 61 YNOKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGRGPDYWGQGTIVTVSS 120
QY 121 GVGSGGGGGSGGGSIDILTQSPAIMSASPGKVTMTCSASSSVSYMHMYOQKSGTSPKR 180
DB 121 GVGSGGGGGSGGGSIDILTQSPAIMSASPGKVTMTCSASSSVSYMHMYOQKSGTSPKR 180
QY 181 WIYDTSKLASGVPRFSGSGGNSYSLTISVEAEDDATYTCQOMSGYPLTFGAGTKLEI 240
DB 181 WIYDTSKLASGVPRFSGSGGNSYSLTISVEAEDDATYTCQOMSGYPLTFGAGTKLEI 240
QY 241 K 241
DB 241 K 241
```

RESULT 3
ABR62132
ID ABR62132 standard; protein; 242 AA.
XX

AC ABR62132;
XX
XX 29-AUG-2003 (first entry)
XX
DE Single chain antibody sequence #SEQ ID 20.
XX
XX Tumour; drug delivery; ligand; cancer; carcinoma; bladder; breast;
XX cervix; colorectum; lung; ovary; pancreas; prostate; stomach;
XX cholangiocarcinoma; gastric sarcoma; glioma; lymphoma; melanoma;
XX multiple myeloma; osteosarcoma; head; neck; radiation; x-ray; antibody.
OS Synthetic.
XX
XX WO2003028640-A2.
XX
XX 10-APR-2003.
XX
XX 27-SEP-2002; 2002WO-US030917.
XX
XX 03-OCT-2001; 2001US-0328123P.
XX
XX (UYVA-) UNIV VANDERBILT.
XX
XX Hallahan DE, Qu S;
XX WPI, 2003-421186/39.
XX
XX Identifying molecule that binds to irradiated tumor in a subject, by
XX exposing tumor to ionizing radiation, administering library of diverse
XX molecules and isolating library molecules from tumor to identify the
XX target.
XX
XX Claim 38; Page 107-108; 108pp; English.
XX
XX The invention relates to a method for identifying a molecule that binds
XX an irradiated tumour in a subject. The method of the invention involves
XX exposing a tumour to ionizing radiation, administering a library of
XX diverse molecules to a subject, and isolating one or more molecules of
XX the library from the tumour. The method of the invention is useful for
XX identifying a molecule that binds an irradiated tumour in a subject e.g.
XX warm-blooded vertebrate and human, and also for tumour detection. The
XX tumour is a primary or a metastasized tumour such as carcinoma of the
XX bladder, breast, cervix, colorectum, lung, ovary, pancreas, prostate,
XX stomach, cholangiocarcinoma, gastric sarcoma, glioma, lymphoma, melanoma,
XX multiple myeloma, osteosarcoma, head and neck tumor and solid tumor. The
XX method of the invention is useful for X-ray-guided delivery of a
XX therapeutic composition, a diagnostic composition or their combinations
XX to a tumour in a subject. The current sequence represents a single chain
XX antibody sequence that was identified following in vivo panning to
XX irradiated tumours. This antibody binds platelet membrane glycoprotein
XX IIB
SQ Sequence 242 AA;
Query Match 80.4%; Score 1025.5; DB 6; Length 242;
Best Local Similarity 81.7%; Pred. No. 9.7e-61;
Matches 196; Conservative 13; Mismatches 30; Indels 1; Gaps 1;
QY 2 OVULOQSGPELEKPGASVYLSCKASGYSPFTGYTMNWKQSHGKSLWMLGLTPYNGASSY 61
DB 3 OVULOQSGPELVKPAASVYKSCASGYFTTSTVMWVWQKQCGLEWMLGYNPNDGRTY 62
QY 62 NQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGRFDYWGQGTITVTS 121
DB 63 NEKFRGKATLTSDKSSSTAYMELSLTSEDSAVYFCARPGYNG-ALDYPWQGTITVTS 121
QY 122 VCGSGGGGGGGGGGSIELTQSPAIMSASBGEKVTTCGASSSVSTMYHYQKSGSPKRW 181
DB 122 GGGSGGGGGGGGGGSIELTQSPAIMSASBGEKVTTCGASSSVSTMYHYQKSGSPKRW 181
QY 182 IYDTSEKLAGVGRFSGSGSGNSYSLTSSVEABDDATYTCQWMSGYPLTFGAGKLEIK 241
DB 182 IYGTSEKLAGVGRFSGSGSGNSYSLTSSVEABDDATYTCQWMSGYPLTFGAGKLEIK 241

RESULT 4
ADT91209
ID ADT91209 standard; protein; 242 AA.
XX
XX ADT91209;
AC
XX 16-DEC-2004 (first entry)
XX
DE Single chain variable fragment (scFv) antibody #2.
XX
XX Tumour; benign intracranial meningioma; arteriovenous malformation;
XX angioma; macular degeneration; melanoma; adenocarcinoma;
XX malignant glioma; prostatic carcinoma; kidney carcinoma;
XX bladder carcinoma; pancreatic carcinoma; thyroid carcinoma;
XX lung carcinoma; colon carcinoma; rectal carcinoma; brain carcinoma;
XX liver carcinoma; breast carcinoma; ovary carcinoma; angiofibroma;
XX retrolental fibroplasia; haemangioma; Kaposi's sarcoma;
XX single chain variable fragment; scFv; antibody.
XX
XX Unidentified.
XX
XX US2004191249-A1.
XX
XX 30-SEP-2004.
XX
XX 20-OCT-2003; 2003US-00689006.
XX
XX 28-APR-2000; 2000WO-US011485.
XX
XX 09-NOV-2001; 2001US-00914605.
XX
XX 27-SEP-2002; 2002US-00259087.
XX
XX (UYVA-) UNIV VANDERBILT.
XX
XX Hallahan DE, Mernaugh R;
XX WPI, 2004-698661/68.
XX
XX N-PSDB; ADT91208.
XX
XX Screening phage-displayed antibodies binding to radiation-inducible
XX neocytogen on cell, comprises contacting cell with antibodies, treating
XX cell with radiation, contacting cell with antibodies not binding to cell,
XX detecting bound antibody.
XX
XX Claim 4; SEQ ID NO 20; 64pp; English.
XX
XX The invention relates to a method for screening phage-displayed
XX antibodies binding to radiation-inducible neocytogen on cell. The method
XX involves contacting cell with antibodies, treating cell with radiation,
XX contacting cell with antibodies not binding to cell and detecting the
XX bound antibody. The method is useful for screening several phage-
XX displayed antibodies for an ability to bind to a radiation-inducible
XX neocytogen present on a cell, where the cell is tumour cell chosen from
XX benign intracranial meningiomas, arteriovenous malformation, angioma,
XX macular degeneration, melanoma, adenocarcinoma, malignant glioma,
XX prostatic carcinoma, kidney carcinoma, bladder carcinoma, pancreatic
XX carcinoma, thyroid carcinoma, lung carcinoma, colon carcinoma, rectal
XX carcinoma, brain carcinoma, liver carcinoma, breast carcinoma, ovary
XX carcinoma, solid tumours, solid tumour metastases, angiofibromas,
XX retrolental fibroplasia, haemangiomas, Kaposi's sarcoma, head and neck
XX carcinomas and their combinations or vascular endothelial cell. The
XX present sequence is a single chain variable fragment (scFv) antibody that
XX binds to radiation-inducible neocytogens.
SQ Sequence 242 AA;
Query Match 80.4%; Score 1025.5; DB 8; Length 242;
Best Local Similarity 81.7%; Pred. No. 9.7e-61;
Matches 196; Conservative 13; Mismatches 30; Indels 1; Gaps 1;
QY 2 OVULOQSGPELEKPGASVYLSCKASGYSPFTGYTMNWKQSHGKSLWMLGLTPYNGASSY 61
DB 2 OVULOQSGPELEKPGASVYLSCKASGYSPFTGYTMNWKQSHGKSLWMLGLTPYNGASSY 61

PT	comprise representation of plaque derived antigens or epitopes on a
PT	display vehicle, and introducing the vehicle into the recipient.
XX	
PS	Example 2; Fig 11; 120pp; English.
XX	
CC	This sequence shows scFv 508F heavy chain, linker and light chain. The
CC	scFv fragment was derived from the 508 IGM hybridoma which is generated
CC	from splenocytes of a mouse that has been immunised with a peptide
CC	corresponding to the 16 amino terminal residues of beta-AP conjugated to
CC	keyhole limpet hemocyanin used a carrier. The resultant variable chain
CC	fragments may be used in the method of the invention. Cys 96 of the VL
CC	fragment was replaced with various amino acids to see if production yield
CC	or stability were effected without having an adverse effect on its
CC	binding affinity. The invention provides an agent for treating a plaque
CC	forming disease. Antigenic polypeptides are displayed on a display
CC	vehicle and are capable of eliciting antibodies capable of disaggregating
CC	the aggregating protein and/or of preventing aggregation of the
CC	aggregating protein. This reduces formation of amyloid plaques in the
CC	brain of victims of plaque forming diseases, e.g. early onset Alzheimer's
CC	disease, late onset Alzheimer's disease, pre-symptomatic Alzheimer's
CC	disease, SMA amyloidosis, hereditary Icelandic syndrome, senility, kuru,
CC	multiple myeloma, scrapie, bovine spongiform encephalopathy (BSE), kuru,
CC	Creutzfeldt-Jakob Disease (CJD), Gerstmann-Strausler-Sheinker Disease
CC	(GSS) and fatal familial insomnia (FFI)
XX	
SQ	Sequence 239 AA:
	Query Match 79.2%; Score 1010.5; DB 4; Length 239;
	Best Local Similarity 79.8%; Pred. No. 9.6e-60;
	Matches 194; Conservative 16; Mismatches 26; Indels 7; Gaps 2;
QY	2 QVQLQSGPELEKRGASVKSLCKRSGYSPFTGYTMNWKSHGKSLRWIGLITPNAGASY 61
DB	1 QVQLQSGAEILVRGVSVKISKSGYTFPDYAHWVKSHSLRWIGLITVYGPASY 60
QY	62 NQKRGKATITVDKSSSTAWMDLLSTSEDSAVYFCARG---GYDGRGPDYWGQGTITV 118
DB	61 NQKRGKATITVDKSSSTAWMDLLSTSEDSAVYFCARGTMSR---FDYWGQVTITV 116
QY	119 SSGVGGSGGGGGGGGSDIELTQSPALMASAPGEEKVTMTCSASSSVSMHWYQOKSGTSP 178
DB	117 SSGGGSGGGGGGGGSDIELTQSPALMASAPGEEKVTMTCSASSSISYMHYQOKPGTSP 176
QY	179 KRWIYDTSKLAGVPGPRFGSGSGNSYSLTISVLEADDAITYYQQMSGPILTGAGTKL 238
DB	177 KRWIYDTSKLAGVPGPRFGSGSGTSTLTISMEADDAITYYCHORSSYPTFGGAKL 236
QY	239 EIK 241
DB	237 EIK 239
RESULT 6	
AA016066	AA016066 standard; protein: 239 AA.
XX	AA016066;
AC	
XX	27-FEB-2003 (first entry)
DT	
XX	Human neurological/CNS disease treatment method-related protein.
DE	
XX	Vaccine; gene therapy; neurological disease; CNS disorder;
KW	central nervous system disorder; olfactory system; Alzheimer's disease;
KW	Creutzfeldt-Jakob disease; Huntington's chorea; Parkinson's disease;
KW	viral infection of the brain; brain tumour; lysosomal storage disease;
KW	multiple sclerosis.
XX	
OS	Homo sapiens.
XX	
PN	WO200274243-A2.
XX	
PD	26-SEP-2002.

XX 15-MAR-2002; 2002WO-US008042.
 PF 15-MAR-2001; 2001US-00808037.
 PR 15-MAR-2001; 2001US-00808037.
 XX (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.
 PA (MCIN/) MCINNIS P.
 XX Solomon B, Frenkel D;
 PI WPI; 2003-040542/03.
 DR N-PSDB; AAL51099.
 XX
 PT Treating or diagnosing neurological diseases of the central nervous
 PT system, e.g. Alzheimer's disease, comprises displaying a polypeptide or
 PT diagnostic agent on viral display vehicle and introducing or detecting
 PT the display vehicle.
 XX
 PS Example 2; Fig 11A; 214pp; English.
 XX
 CC The invention comprises a method for treating a neurological disease or a
 CC central nervous system (CNS) disorder. The method involves displaying a
 CC therapeutic molecule capable of treating the neurological disease or CNS
 CC disorder on a viral display vehicle. The viral display vehicle is then
 CC introduced into the olfactory system of a subject to treat the disease or
 CC disorder. The method of the invention is useful for preventing, treating
 CC and diagnosing neurological diseases or CNS disorders, such as:
 CC Alzheimer's disease; Creutzfeldt-Jakob disease; Huntington's chorea; viral
 CC infections of the brain; brain tumours; lysosomal storage diseases;
 CC Parkinson's disease; and multiple sclerosis. The present amino acid
 CC sequence represents a protein which was used in the invention
 XX
 SQ Sequence 239 AA;

Query Match 79.2%; Score 1010.5; DB 6; Length 239;
 Best Local Similarity 79.8%; Pred. No. 9.6e-60;
 Matches 194; Conservative 16; Mismatches 26; Indels 7; Gaps 2;

QY 2 QVQLQSGPELEKPGASVKLSCKASGYSTGYTMMWVKQSGKSLIEWIGLITPNGASSY 61
 DB 1 QVQLQSGPELEKPGASVKLSCKASGYSTGYTMMWVKQSGKSLIEWIGLITPNGASSY 60
 QY 62 NQKFRGKATLTVDKSSSTAYMDLSTLSEDSAVYFCARG--GYGRGPDVWGQGTITV 118
 DB 61 NQKFRGKATLTVDKSSSTAYMDLSTLSEDSAVYFCARG--GYGRGPDVWGQGTITV 116
 QY 119 SSGVGGSGGGSGGSDIELTQSPAIMSASPGKVTMTCSASSSVSYVMWYQKSGTSP 178
 DB 117 SSGVGGSGGGSGGSDIELTQSPAIMSASPGKVTMTCSASSSVSYVMWYQKSGTSP 176
 QY 179 KRWITDTSKLASGVPRPSGGSGNSYSITLTSVEAEDDARYYCOQMGYPITFGAGTKL 238
 DB 177 KRWITDTSKLASGVPRPSGGSGNSYSITLTSVEAEDDARYYCOQMGYPITFGAGTKL 236
 QY 239 EIK 241
 DB 237 EIK 239
 RESULT 7
 ID ADJ88113 standard; protein; 239 AA.
 AC ADJ88113;
 XX 06-MAY-2004 (first entry)
 DE Human beta amyloid peptide antibody (508) heavy chain protein.
 XX Neurological disease; central nervous system; CNS disorder;
 KM plaque-forming disease; Alzheimer's disease; SAA amyloidosis;
 KM hereditary Icelandic syndrome; senility; multiple myeloma; scrapie;
 KM bovine spongiform encephalopathy; BSE; kuru; Creutzfeldt-Jakob disease;

KW CJD; Gerstmann-Strausler-Sheinker disease; GSS; fatal familial insomnia;
 KM PFI; non-plaque-forming disease; Huntington's chorea; viral infection;
 KM brain tumour; lysosomal storage disease; neurodegeneration;
 KM multiple sclerosis; vaccine; beta amyloid peptide; beta AP; antibody;
 KM human.
 XX Homo sapiens.
 OS
 XX
 PH Key Location/Qualifiers
 FT Region 31..35
 FT /note= "CDR1"
 FT Region 50..66
 FT /note= "CDR2"
 FT Region 99..107
 FT /note= "CDR3"
 XX
 PN US2004013647-A1.
 XX
 PD 22-JAN-2004.
 XX
 PF 11-MAR-2003; 2003US-00384788.
 XX
 PR 03-SEP-1999; 99US-0152417P.
 PR 29-DEC-1999; 99US-00473653.
 PR 31-JUL-2000; 2000US-00629971.
 PR 31-AUG-2000; 2000WO-11000518.
 PR 15-MAR-2001; 2001US-00808037.
 PR 07-AUG-2001; 2001US-00830954.
 PR 12-APR-2002; 2002US-0371735P.
 PR 06-JUN-2002; 2002US-00162889.
 XX
 PA (UYRA-) UNIV RAMOT AT TEL AVIV LTD.
 XX
 PI Solomon B, Frenkel D;
 XX WPI; 2004-106188/11.
 DR N-PSDB; ADJ88112.
 XX

PT Treating neurological disease CNS e.g., Alzheimer's disease, by
 PT displaying therapeutic molecule capable of treating the disease on viral
 PT display vehicle which is then administered to subject through olfactory
 PT system.

PS Example 2; SEQ ID NO 6; 68pp; English.

CC The invention relates to a method of treating a neurological disease or
 CC disorder of the central nervous system (CNS). The method involves
 CC displaying a therapeutic molecule capable of treating the neurological
 CC disease or disorder of the CNS on a viral display vehicle and introducing
 CC viral display vehicle into a subject by applying an effective amount of
 CC the viral display vehicle displaying the therapeutic molecule to an
 CC olfactory system of the subject. The method is useful for treating a
 CC neurological disease or disorder of CNS such as a plaque-forming disease
 CC such as Alzheimer's disease, late onset Alzheimer's disease,
 CC presymptomatic Alzheimer's disease, SAA amyloidosis, hereditary Icelandic
 CC syndrome, senility, multiple myeloma, scrapie, bovine spongiform
 CC encephalopathy (BSE), kuru, Creutzfeldt-Jakob disease (CJD), Gerstmann-
 CC Strussler-Sheinker disease (GSS) or fatal familial insomnia (PFI). The
 CC method is also useful for treating a non plaque forming disease or
 CC disorder e.g. Huntington's chorea, viral infections of the brain, brain
 CC tumours, lysosomal storage diseases which cause neurodegeneration and are
 CC manifested by enzyme deficiencies and multiple sclerosis. The invention
 CC is also used in the preparation of vaccines. The present sequence is
 CC human beta amyloid peptide (beta AP) antibody heavy chain protein. This
 CC sequence is used to illustrate the method of the invention.

SO Sequence 239 AA;

Query Match 79.2%; Score 1010.5; DB 8; Length 239;
 Best Local Similarity 79.8%; Pred. No. 9.6e-60;
 Matches 194; Conservative 16; Mismatches 26; Indels 7; Gaps 2;

QY 2 QVQLQSGPELEKPGASVKLSCKASGYSTGYTMMWVKQSGKSLIEWIGLITPNGASSY 61

Db 1 QVKKQSSGAEIWRPVSVKISCKSGSYFTFDAMHWVQSHKSLIEMIGVISTYYGDASY 60
QY 62 NQFRGKATLTVDKSSSTAYMDLSTLSEDSAVYFCARG--GYDGRGFYWGQGTITTV 118
Db 61 NQFRGKATLTVDKSSSTAYMDLSTLSEDSAVYFCARGATMSY----FDVWGQVITTV 116
QY 119 SSGVGGSGGGGGGGSDIELTQSPALMSASPGKRYMTCSASSSVSYMHYQOKSGTSP 178
Db 117 SSGGGGGGGGGGGSDIELTQSPALMSASPGKRYMTCSASSSVSYMHYQOKSGTSP 176
QY 179 KMWYDTSLKASGVGRFSGSGSGSYSLTSSVEAEDATYYCOOMSGYPLTFGAGTKL 238
Db 177 KMWYDTSLKASGVGRFSGSGSGSYSLTSSVEAEDATYYCOOMSGYPLTFGAGTKL 236
QY 239 EIK 241
Db 237 EIK 239

RESULT 8
ADV66089
ID ADV66089 standard; protein; 494 AA.

AC ADV66089;
DT 24-FEB-2005 (first entry)
XX
XX
DE Anti-CD3-anti-EpCAM bispecific single chain antibody - SEQ ID 12.

KW bispecific single chain antibody; epithelial cell adhesion molecule;
KW EpCAM; CD3; tumor; cancer; cytostatic.

OS Unidentified.

PN WO2004106383-A1.

PD 09-DEC-2004.

PF 26-MAY-2004; 2004WO-EP005687.

PR 31-MAY-2003; 2003EP-00012133.

PR 31-MAY-2003; 2003EP-00012134.

PA (MICR-) MICROMET AG.

PI Kufer P, Berry M, Offner S, Brischwein K, Wolf A, Raum T;

PI Kohleisen B, Lenkner-Schuetz U, Baerle P;

DR WPI; 2005-021271/02.

DR N-PSDB; ADV66088.

PT New pharmaceutical composition having a bispecific single chain antibody
PT construct, useful for preventing, treating or ameliorating a tumorous
PT disease, such as an epithelial or minimal residual cancer.

PS Claim 12; SEQ ID NO 12; 227bp; English.

XX The invention comprises a composition that contains a bispecific single
XX chain antibody consisting of at least two domains, where one of domains
XX binds to human epithelial cell adhesion molecule (EpCAM) antigen, and the
XX second domain binds to human CD3 antigen. The bispecific antibody
XX construct of the invention is useful for the prevention, treatment or
XX amelioration of a tumorous disease, such as an epithelial or minimal
XX residual cancer. The present amino acid sequence represents a bispecific
XX single chain antibody of the invention.

XX Sequence 494 AA;

Query Match 78.7%; Score 1004; DB 9; Length 494;
Best Local Similarity 80.3%; Pred. No. 5.5e-59;
Matches 192; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

QY 3 VOLQSGPELEKPGASVYKLSCKASGYFTGYTMWVQSHKSLIEMIGLITPYNGASSYN 62
Db 2 IKLQSSGAEIWRPVSVKISCKSGSYFTFDAMHWVQSHKSLIEMIGVISTYYGDASY 61
QY 63 NQFRGKATLTVDKSSSTAYMDLSTLSEDSAVYFCARGGYDGRGFYWGQGTITTVSSGV 122
Db 62 NQFRGKATLTVDKSSSTAYMDLSTLSEDSAVYFCARGYDHYCLDYWGQGTITTVSSGG 121
QY 123 GSGGGGGGGGGGGSDIELTQSPALMSASPGKRYMTCSASSSVSYMHYQOKSGTSPRWT 182
Db 122 GSGGGGGGGGGGGSDIELTQSPALMSASPGKRYMTCSASSSVSYMHYQOKSGTSPRWT 181
QY 183 YDTSKVASGVGRFSGSGSGSYSLTSSVEAEDATYYCOOMSGYPLTFGAGTKLEIK 241
Db 182 YDTSKVASGVGRFSGSGSGSYSLTSSVEAEDATYYCOOMSGYPLTFGAGTKLEIK 240

RESULT 9
ADV66137
ID ADV66137 standard; protein; 500 AA.

AC ADV66137;

DT 24-FEB-2005 (first entry)

DE Anti-CD3-anti-EpCAM bispecific single chain antibody - SEQ ID 60.

KW bispecific single chain antibody; epithelial cell adhesion molecule;
KW EpCAM; CD3; tumor; cancer; cytostatic.

OS Unidentified.

PN WO2004106383-A1.

PD 09-DEC-2004.

PF 26-MAY-2004; 2004WO-EP005687.

PR 31-MAY-2003; 2003EP-00012133.

PR 31-MAY-2003; 2003EP-00012134.

PA (MICR-) MICROMET AG.

PI Kufer P, Berry M, Offner S, Brischwein K, Wolf A, Raum T;

PI Kohleisen B, Lenkner-Schuetz U, Baerle P;

DR WPI; 2005-021271/02.

DR N-PSDB; ADV66136.

PT New pharmaceutical composition having a bispecific single chain antibody
PT construct, useful for preventing, treating or ameliorating a tumorous
PT disease, such as an epithelial or minimal residual cancer.

PS Claim 12; SEQ ID NO 60; 227bp; English.

XX The invention comprises a composition that contains a bispecific single
XX chain antibody consisting of at least two domains, where one of domains
XX binds to human epithelial cell adhesion molecule (EpCAM) antigen, and the
XX second domain binds to human CD3 antigen. The bispecific antibody
XX construct of the invention is useful for the prevention, treatment or
XX amelioration of a tumorous disease, such as an epithelial or minimal
XX residual cancer. The present amino acid sequence represents a bispecific
XX single chain antibody of the invention.

XX Sequence 500 AA;

Query Match 78.7%; Score 1004; DB 9; Length 500;
Best Local Similarity 80.3%; Pred. No. 5.6e-59;
Matches 192; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

QY 3 VOLQSGPELEKPGASVYKLSCKASGYFTGYTMWVQSHKSLIEMIGLITPYNGASSYN 62
Db 2 IKLQSSGAEIWRPVSVKISCKSGSYFTFDAMHWVQSHKSLIEMIGVISTYYGDASY 61

QY 63 QKFRKATLTVDKSSSTAYMDLSTLSEDSAVYFCARGGYDGRGFDYWGQGTTVVSSGV 122
DB 62 QKFKKATLTVDKSSSTAYMDLSTLSEDSAVYFCARYDDHYCLDYWGQGTTLTVSSGG 121
QY 123 GSGGGGGGGGGSDIELTQSPAIMSASPEKVTMTCSASSSVYMWYQKSGTSPKRWI 182
DB 122 GSGGGGGGGGGSDIQLTQSPAIMSASPEKVTMTCRASSSVYMWYQKSGTSPKRWI 181
QY 183 YDTSKASGVPRFSGSGSGNSYSLTSSVEAEDDATYTCQWMSGYPLTFGAGTLEIK 241
DB 182 YDTSKASGVPRFSGSGSGTSTLSSMEAEADATYTCQWMSGNPLTFGAGTLEIK 240

RESULT 10
ADV66095
ID ADV66095 standard; protein; 500 AA.
AC ADV66095;
XX 24-FEB-2005 (first entry)
DT 24-FEB-2005 (first entry)
DE Anti-CD3-anti-EpCAM bispecific single chain antibody - SEQ ID 18.
XX bispecific single chain antibody; epithelial cell adhesion molecule;
KW EpCAM; CD3; tumor; cancer; cytostatic.
XX Unidentified.
OS WO2004106383-A1.
XX PN 09-DEC-2004.
XX PD 26-MAY-2004; 2004WO-EP005687.
XX PF 31-MAY-2003; 2003EP-00012133.
XX PR 31-MAY-2003; 2003EP-00012134.
XX PA (MICR-) MICROMET AG.
XX PI Kufer P, Berry M, Offner S, Brischwein K, Wolf A, Raum T;
XX PI Kohleisen B, Lenkkeri-Schuetz U, Baerle P;
XX DR WPI; 2005-021271/02.
XX DR N-PSDB; ADV66094.
XX PT New pharmaceutical composition having a bispecific single chain antibody
XX PT construct, useful for preventing, treating or ameliorating a tumorous
XX PT disease, such as an epithelial or minimal residual cancer.
XX PS Claim 12; SEQ ID NO 18; 227pp; English.
XX CC The invention comprises a composition that contains a bispecific single
XX CC chain antibody consisting of at least two domains, where one of domains
XX CC binds to human epithelial cell adhesion molecule (EpCAM) antigen, and the
XX CC second domain binds to human CD3 antigen. The bispecific antibody
XX CC construct of the invention is useful for the prevention, treatment or
XX CC amelioration of a tumorous disease, such as an epithelial or minimal
XX CC residual cancer. The present amino acid sequence represents a bispecific
XX CC single chain antibody of the invention.
SQ Sequence 500 AA;

Query Match 78.7%; Score 1004; DB 9; Length 500;
Best Local Similarity 80.3%; Pred. No. 5.6e-59;
Matches 192; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

QY 3 VOLQSGPELEKPGASVYLSCASGYSTGYTMVWKSHGSLWIGLITPYNGASSYN 62
DB 2 IKLQSGELARPGASVYMSCKTSGYFTTRTYMHWKQPGQGLWIGYINPSRGYTYN 61
QY 63 QKFRKATLTVDKSSSTAYMDLSTLSEDSAVYFCARGGYDGRGFDYWGQGTTVVSSGV 122
DB 62 QKFKKATLTVDKSSSTAYMDLSTLSEDSAVYFCARYDDHYCLDYWGQGTTLTVSSGG 121

DB 62 QKFKKATLTVDKSSSTAYMDLSTLSEDSAVYFCARYDDHYCLDYWGQGTTLTVSSGG 121
QY 123 GSGGGGGGGGGSDIELTQSPAIMSASPEKVTMTCSASSSVYMWYQKSGTSPKRWI 182
DB 122 GSGGGGGGGGGSDIQLTQSPAIMSASPEKVTMTCRASSSVYMWYQKSGTSPKRWI 181
QY 183 YDTSKASGVPRFSGSGSGNSYSLTSSVEAEDDATYTCQWMSGYPLTFGAGTLEIK 241
DB 182 YDTSKASGVPRFSGSGSGTSTLSSMEAEADATYTCQWMSGNPLTFGAGTLEIK 240

RESULT 11
ADV66097
ID ADV66097 standard; protein; 500 AA.
AC ADV66097;
XX 24-FEB-2005 (first entry)
DT 24-FEB-2005 (first entry)
DE Anti-CD3-anti-EpCAM bispecific single chain antibody - SEQ ID 20.
XX bispecific single chain antibody; epithelial cell adhesion molecule;
KW EpCAM; CD3; tumor; cancer; cytostatic.
XX Unidentified.
OS WO2004106383-A1.
XX FN 09-DEC-2004.
XX PD 26-MAY-2004; 2004WO-EP005687.
XX PF 31-MAY-2003; 2003EP-00012133.
XX PR 31-MAY-2003; 2003EP-00012134.
XX PA (MICR-) MICROMET AG.
XX PI Kufer P, Berry M, Offner S, Brischwein K, Wolf A, Raum T;
XX PI Kohleisen B, Lenkkeri-Schuetz U, Baerle P;
XX DR WPI; 2005-021271/02.
XX DR N-PSDB; ADV66096.
XX PT New pharmaceutical composition having a bispecific single chain antibody
XX PT construct, useful for preventing, treating or ameliorating a tumorous
XX PT disease, such as an epithelial or minimal residual cancer.
XX PS Claim 12; SEQ ID NO 20; 227pp; English.
XX CC The invention comprises a composition that contains a bispecific single
XX CC chain antibody consisting of at least two domains, where one of domains
XX CC binds to human epithelial cell adhesion molecule (EpCAM) antigen, and the
XX CC second domain binds to human CD3 antigen. The bispecific antibody
XX CC construct of the invention is useful for the prevention, treatment or
XX CC amelioration of a tumorous disease, such as an epithelial or minimal
XX CC residual cancer. The present amino acid sequence represents a bispecific
XX CC single chain antibody of the invention.
SQ Sequence 500 AA;

Query Match 78.7%; Score 1004; DB 9; Length 500;
Best Local Similarity 80.3%; Pred. No. 5.6e-59;
Matches 192; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

QY 3 VOLQSGPELEKPGASVYLSCASGYSTGYTMVWKSHGSLWIGLITPYNGASSYN 62
DB 2 IKLQSGELARPGASVYMSCKTSGYFTTRTYMHWKQPGQGLWIGYINPSRGYTYN 61
QY 63 QKFRKATLTVDKSSSTAYMDLSTLSEDSAVYFCARGGYDGRGFDYWGQGTTVVSSGV 122
DB 62 QKFKKATLTVDKSSSTAYMDLSTLSEDSAVYFCARYDDHYCLDYWGQGTTLTVSSGG 121
QY 123 GSGGGGGGGGGSDIELTQSPAIMSASPEKVTMTCSASSSVYMWYQKSGTSPKRWI 182

Db 122 GGGGGGGGGGSDIQLTQSPALMSASPEKVTMTCRASSSVSYMMWYQKSGTSPKRWI 181
OY 183 YDTSKIASGVPRFSGSGSGNSYSLTISVEAEDATYYCOQMSGYPLTFGAGTKLEIK 241
Db 182 YDTSKVASGVPRFSGSGSGTSLTISMEADATYYCCQMSNPITFGAGTKLEIK 240

RESULT 12
ADV6131
ID ADV6131 standard; protein; 503 AA.

AC ADV6131;
XX
XX
XX 24-FEB-2005 (first entry)
DT
XX
XX Anti-CD3-anti-EpCAM bispecific single chain antibody - SEQ ID 54.
DE
XX bispecific single chain antibody; epithelial cell adhesion molecule;
KW EpCAM; CD3; tumor; cancer; cytostatic.
XX
XX Unidentified.

OS
XX WO2004106383-A1.
XX
XX 09-DEC-2004.
XX
XX 26-MAY-2004; 2004WO-EP005687.
XX
XX 31-MAY-2003; 2003EP-00012133.
XX 31-MAY-2003; 2003EP-00012134.
XX
XX (MICR-) MICROMET AG.

PI Kufer P, Berry M, Offner S, Brischwein K, Wolf A, Raum T;
PI Kohleisen B, Lenkeri-Schuetz U, Baerle P;
XX WPI; 2005-021271/02.
XX
XX N-PSDB; ADV6130.

PT New pharmaceutical composition having a bispecific single chain antibody
PT construct, useful for preventing, treating or ameliorating a tumorous
PT disease, such as an epithelial or minimal residual cancer.

PS Claim 12; SEQ ID NO 54; 227bp; English.

XX The invention comprises a composition that contains a bispecific single
XX chain antibody consisting of at least two domains, where one of domains
XX binds to human epithelial cell adhesion molecule (EpCAM) antigen, and the
XX second domain binds to human CD3 antigen. The bispecific antibody
XX construct of the invention is useful for the prevention, treatment or
XX amelioration of a tumorous disease, such as an epithelial or minimal
XX residual cancer. The present amino acid sequence represents a bispecific
XX single chain antibody of the invention.

XX Sequence 503 AA;

Query Match 78.7%; Score 1004; DB 9; Length 503;
Best Local Similarity 80.3%; Pred. No. 5.6e-59;
Matches 192; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

OY 3 VOLQOOGPELEKPGASVYLSCASGYSTGYTMWVYQSHGKSLWIGLITPYNGASSYN 62
Db 2 IKLQOGGELARPGASVVMCKTSGYTFRTYTMWVKRPFQGLEWIGYINPSRGYTYN 61
OY 63 QKFKGKATLTVDKSSSTAYMDLSLTSFDSAVYFCARGYDGRGFDYWGQTTVTVSSGV 122
Db 62 QKFKDVAITLTDKSSSTAYMQLSLTSFDSAVYFCARYDDHYCLDWGQTTLVSSGG 121
OY 123 GSGGGGGGGGSDIELTQSPALMSASPEKVTMTCSASSSVSYMMWYQKSGTSPKRWI 182
Db 122 GSGGGGGGGGSDIQLTQSPALMSASPEKVTMTCRASSSVSYMMWYQKSGTSPKRWI 181

OY 183 YDTSKIASGVPRFSGSGSGNSYSLTISVEAEDATYYCOQMSGYPLTFGAGTKLEIK 241
Db 182 YDTSKVASGVPRFSGSGSGTSLTISMEADATYYCOQMSNPITFGAGTKLEIK 240

RESULT 13
ADV6093
ID ADV6093 standard; protein; 503 AA.

AC ADV6093;
XX
XX 24-FEB-2005 (first entry)
DT
XX
XX Anti-CD3-anti-EpCAM bispecific single chain antibody - SEQ ID 16.
DE
XX bispecific single chain antibody; epithelial cell adhesion molecule;
KW EpCAM; CD3; tumor; cancer; cytostatic.
XX
XX Unidentified.

OS
XX WO2004106383-A1.
XX
XX 09-DEC-2004.
XX
XX 26-MAY-2004; 2004WO-EP005687.
XX
XX 31-MAY-2003; 2003EP-00012133.
XX 31-MAY-2003; 2003EP-00012134.
XX
XX (MICR-) MICROMET AG.

PI Kufer P, Berry M, Offner S, Brischwein K, Wolf A, Raum T;
PI Kohleisen B, Lenkeri-Schuetz U, Baerle P;
XX WPI; 2005-021271/02.
XX
XX N-PSDB; ADV6092.

PT New pharmaceutical composition having a bispecific single chain antibody
PT construct, useful for preventing, treating or ameliorating a tumorous
PT disease, such as an epithelial or minimal residual cancer.

PS Claim 12; SEQ ID NO 16; 227bp; English.

XX The invention comprises a composition that contains a bispecific single
XX chain antibody consisting of at least two domains, where one of domains
XX binds to human epithelial cell adhesion molecule (EpCAM) antigen, and the
XX second domain binds to human CD3 antigen. The bispecific antibody
XX construct of the invention is useful for the prevention, treatment or
XX amelioration of a tumorous disease, such as an epithelial or minimal
XX residual cancer. The present amino acid sequence represents a bispecific
XX single chain antibody of the invention.

XX Sequence 503 AA;

Query Match 78.7%; Score 1004; DB 9; Length 503;
Best Local Similarity 80.3%; Pred. No. 5.6e-59;
Matches 192; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

OY 3 VOLQOOGPELEKPGASVYLSCASGYSTGYTMWVYQSHGKSLWIGLITPYNGASSYN 62
Db 2 IKLQOGGELARPGASVVMCKTSGYTFRTYTMWVKRPFQGLEWIGYINPSRGYTYN 61
OY 63 QKFKGKATLTVDKSSSTAYMDLSLTSFDSAVYFCARGYDGRGFDYWGQTTVTVSSGV 122
Db 62 QKFKDVAITLTDKSSSTAYMQLSLTSFDSAVYFCARYDDHYCLDWGQTTLVSSGG 121
OY 123 GSGGGGGGGGSDIELTQSPALMSASPEKVTMTCSASSSVSYMMWYQKSGTSPKRWI 182
Db 122 GSGGGGGGGGSDIQLTQSPALMSASPEKVTMTCRASSSVSYMMWYQKSGTSPKRWI 181
OY 183 YDTSKIASGVPRFSGSGSGNSYSLTISVEAEDATYYCOQMSGYPLTFGAGTKLEIK 241
Db 182 YDTSKVASGVPRFSGSGSGTSLTISMEADATYYCCQMSNPITFGAGTKLEIK 240

RESULT 14

ADV66091

ID ADV66091 standard; protein; 503 AA.

AC ADV66091;

DT 24-FEB-2005 (first entry)

DE Anti-CD3-anti-EpCAM bispecific single chain antibody - SEQ ID 14.

KM bispecific single chain antibody; epithelial cell adhesion molecule; EpCAM; CD3; tumor; cancer; cytostatic.

OS Unidentified.

PN WO2004106381-A1.

PD 09-DEC-2004.

PF 26-MAY-2004; 2004WO-EP005687.

PR 31-MAY-2003; 2003EP-00012133.

PR 31-MAY-2003; 2003EP-00012134.

XX (MICR-) MICROMET AG.

XX Kufer P, Berry M, Offner S, Brieschwein K, Wolf A, Raum T;

XX PI Kohleisen B, Lenkner-Schuetz U, Baerle P;

XX DR WPI; 2005-021271/02.

XX DR N-PSDB; ADV66090.

XX New pharmaceutical composition having a bispecific single chain antibody construct, useful for preventing, treating or ameliorating a tumorous disease, such as an epithelial or minimal residual cancer.

PS Claim 12; SEQ ID NO 14; 227PP; English.

XX The invention comprises a composition that contains a bispecific single chain antibody consisting of at least two domains, where one of domains binds to human epithelial cell adhesion molecule (EpCAM) antigen, and the second domain binds to human CD3 antigen. The bispecific antibody construct of the invention is useful for the prevention, treatment or amelioration of a tumorous disease, such as an epithelial or minimal residual cancer. The present amino acid sequence represents a bispecific single chain antibody of the invention.

SQ Sequence 503 AA;

Query Match 78.7%; Score 1004; DB 9; Length 503;

Best Local Similarity 80.3%; Pred. No. 5,6e-59;

Matches 192; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

QY 3 VOLQSGPFLKPKASVKLSKASGYSFTGYMMWKSHGSLKLTITTYNGASSTN 62

DB 2 IRLQSGALARPASVSKMSCKTSGYTFRTYTWKORPGGLEWIGYINFSRGTYNTN 61

QY 63 QKFRGATLTIVKSSSTAYMDLLSLTSEDSAVYFCARGYDGRGPDYMGQGTWTVSSGV 122

DB 62 QKFRGATLTIVKSSSTAYMDLLSLTSEDSAVYFCARGYDGRGPDYMGQGTWTVSSGV 121

QY 123 GSGGGGSGGGSDIELTQSPAIMSAPBEKVTMTCSASSSVSYMMWYQKSGTSPKRWI 182

DB 122 GSGGGGSGGGSDIELTQSPAIMSAPBEKVTMTCSASSSVSYMMWYQKSGTSPKRWI 181

QY 183 YQTSKASGVPGRFSSGSGNSLITSSVEABDATTYCCQWSGTPLTFGAGTKLEIK 241

DB 182 YQTSKASGVPGRFSSGSGNSLITSSVEABDATTYCCQWSGTPLTFGAGTKLEIK 240

RESULT 15

ADV14540

ID ADV14540 standard; protein; 503 AA.

AC ADV14540;

DT 24-FEB-2005 (first entry)

DE Bispecific VH(CD3)-VL(CD3)-VL(CD19)-VH(CD19) antibody protein Seq 14.

KM bispecific antibody; antibody engineering; antibody therapy; CD3; CD19; proliferative disorders; cancer; tumor; B-cell leukemia; inflammation;

KM immune disorder; autoimmune disease; rheumatoid arthritis;

KM viral infection; allergy; parasitic infection; graft-versus-host disease; cytostatic; antiinflammatory; immunosuppressive; antineoplastic; antiarthritic; antiallergic.

KM antineumatic; antiarthritic; virucide; antiparasitic; antiallergic.

OS Homo sapiens.

PN WO2004106381-A1.

PD 09-DEC-2004.

PF 26-MAY-2004; 2004WO-EP005685.

PR 31-MAY-2003; 2003EP-00012136.

XX (MICR-) MICROMET AG.

XX Kufer P, Lutterbuese R, Kohleisen B, Zeman S, Baerle P;

XX PI WPI; 2005-021270/02.

XX DR N-PSDB; ADV14539.

XX Use of bispecific single chain antibody construct, nucleic acid sequence encoding the antibody construct, vector containing the nucleic acid or host transformed with the vector for the treatment of e.g. proliferative and autoimmune disease.

PS Claim 9; SEQ ID NO 14; 115PP; English.

XX This invention relates to novel pharmaceutical compositions that comprise a bispecific single chain antibody construct, a nucleic acid sequence encoding the antibody construct and a vector that contains the nucleic acid sequence. Specifically, it refers to an antibody construct that contains binding domains specific for the human T cell differentiation antigens CD3 and CD19, with specific variable heavy and light chain regions. In particular such constructs include, from the N- to C-terminal, in the order, VH(CD19)-VL(CD19)-VH(CD3)-VL(CD3)-VH(CD19)-VL(CD19), or VH(CD3)-VL(CD3)-VL(CD19)-VH(CD19). The present invention describes a method of culturing the host transformed with this vector in order to recover expressed bispecific single chain antibodies from the culture solution. Note that the pharmaceutical composition additionally comprises a proteinaceous compound that provides an activation signal for immune effector cells. Furthermore, this invention provides compositions that can be used for the treatment, prevention or amelioration of proliferative disease, minimal residual cancer, tumorous disease (e.g. B-cell leukemia), inflammatory disease, immunological disorder, autoimmune disease (e.g. rheumatoid arthritis), infectious disease, viral disease, allergic reactions, parasitic reactions, graft-versus-host diseases, host versus-graft diseases and B-cell malignancies. As such, these compositions exhibit cytostatic, antiinflammatory, immunosuppressive, antimicrobial, antineumatic, antiarthritic, virucide, antiparasitic and antiallergic activities. In addition, these compositions provide well-tolerated and convenient medicaments that are highly active and potent at low concentrations and as such avoid adverse side effects including hypersensitivity and inflammatory events caused by excessive protein concentrations. This polypeptide sequence is a bispecific single chain antibody protein that targets human CD3 and CD19 antigens, as given in an exemplification of the invention.

SQ Sequence 503 AA;

Query Match 78.7%; Score 1004; DB 9; Length 503;
 Best Local Similarity 80.3%; Pred. No. 5, 6e-59;
 Matches 192; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

QY	3	VOLQSGPELEKPGASVYKLSCKASGYSTFTGTMNWKQSHGKSLIEWIGLITPYNGASSYN	62
		::: : : : : : : : : :	
Db	2	IKLQSGAEIARPGASVYKMSCKTSGYTFRTYTMHWKORPGGLEWIGINPSRGYTNYN	61
QY	63	QKFRGKATLTVDKSSSTAYMDLISLTSFDSAVYFCARGGYDGRGFPDYMGGTTTVSSGV	122
		: : : : : : : : :	
Db	62	QKFKDKATLTVDKSSSTAYMDLISLTSFDSAVYFCARGGYDGRGFPDYMGGTTTVSSGV	121
QY	123	GSGGGGGGGGGSDIELTQSPAIMSAPGKVTMTCSASSSVSYMHWTQOKSGTSPKRWI	182
		: : : : : : : :	
Db	122	GSGGGGGGGGGSDIQLTQSPAIMSAPGKVTMTCSASSSVSYMHWTQOKSGTSPKRWI	181
QY	183	YDTSKIASGVPGRFSGSGSGNSYSLTISVEAEDDATYYCCQWMSGYPLTFGAGTKLEIK	241
		: : : : : : : :	
Db	182	YDTSKVASGVPYRFSGSGSGTSLTISMEAEADATYYCCQWSSNPLTFGAGTKLEIK	240

Search completed: April 3, 2006, 05:35:30
 Job time : 324 secs

GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: April 3, 2006, 05:30:32 ; Search time 61 Seconds
(without alignments)
1650.768 Million cell updates/sec

Title: US-09-979-539-1

Perfect score: 1276
Sequence: 1 MGVQLQSGPELEKPGASVK.....CQWMSGYPLTFGATKLEIK 241

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: Published Applications AA Main:

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2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep:*
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6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1274	99.8	241	US-10-973-718-5	Sequence 5, Appl
2	1025.5	80.4	242	US-10-259-087A-20	Sequence 20, Appl
3	1025.5	80.4	242	US-10-689-006-20	Sequence 20, Appl
4	1010.5	79.2	239	US-09-808-037-6	Sequence 6, Appl
5	1010.5	79.2	239	US-10-162-889-6	Sequence 6, Appl
6	1010.5	79.2	239	US-10-384-788-6	Sequence 6, Appl
7	1010.5	79.2	239	US-10-618-856-6	Sequence 6, Appl
8	1010.5	79.2	239	US-10-749-522-6	Sequence 6, Appl
9	1010.5	79.2	239	US-11-073-526-6	Sequence 6, Appl
10	1003	78.5	261	US-10-689-006-24	Sequence 24, Appl
11	989.5	77.5	242	US-10-259-087A-18	Sequence 18, Appl
12	989.5	77.5	242	US-10-689-006-18	Sequence 18, Appl
13	967.5	75.8	492	US-10-682-845-63	Sequence 63, Appl
14	967.5	75.8	492	US-10-682-845-79	Sequence 79, Appl
15	967.5	75.8	492	US-10-682-845-83	Sequence 83, Appl
16	966.5	75.7	492	US-10-682-845-87	Sequence 87, Appl
17	966	75.7	246	US-10-861-617-15	Sequence 15, Appl
18	965.5	75.7	492	US-10-682-845-61	Sequence 61, Appl
19	965.5	75.7	492	US-10-682-845-71	Sequence 71, Appl
20	965.5	75.7	492	US-10-682-845-73	Sequence 73, Appl
21	965.5	75.7	492	US-10-682-845-77	Sequence 77, Appl
22	964.5	75.6	409	US-10-966-406-2	Sequence 2, Appl
23	964.5	75.6	409	US-10-362-591-2	Sequence 2, Appl
24	964.5	75.6	492	US-10-682-845-59	Sequence 59, Appl
25	964.5	75.6	492	US-10-682-845-67	Sequence 67, Appl
26	964.5	75.6	492	US-10-682-845-69	Sequence 69, Appl
27	964.5	75.6	499	US-10-805-177-111	Sequence 111, Appl

28	964.5	75.6	500	US-10-168-809-22	Sequence 22, Appl
29	963.5	75.5	492	US-10-682-845-75	Sequence 75, Appl
30	963.5	75.5	492	US-10-682-845-85	Sequence 85, Appl
31	962.5	75.4	260	US-10-435-614-20	Sequence 20, Appl
32	961	75.3	246	US-10-861-617-17	Sequence 17, Appl
33	961	75.3	657	US-10-723-003-48	Sequence 48, Appl
34	961	75.3	657	US-11-004-639-48	Sequence 48, Appl
35	960.5	75.3	492	US-10-682-845-65	Sequence 65, Appl
36	959.5	75.2	256	US-10-247-488-2	Sequence 2, Appl
37	959.5	75.2	258	US-10-247-488-4	Sequence 4, Appl
38	957.5	75.0	492	US-10-682-845-81	Sequence 81, Appl
39	956.5	75.0	495	US-09-948-004-18	Sequence 18, Appl
40	956.5	75.0	495	US-10-672-932-18	Sequence 18, Appl
41	956	74.9	281	US-10-112-788-9	Sequence 9, Appl
42	956	74.9	281	US-10-435-614-15	Sequence 15, Appl
43	948.5	74.3	438	US-10-244-821-88	Sequence 88, Appl
44	948.5	74.3	260	US-10-435-614-19	Sequence 19, Appl
45	941.5	73.8	423	US-10-013	Sequence 8, Appl

ALIGNMENTS

RESULT 1					
US-10-973-718-5					
Sequence 5, Application US/10973718					
Publication No. US20050214304A1					
GENERAL INFORMATION:					
APPLICANT: Pastan, Ira H.					
APPLICANT: Chowdhury, Patha S.					
APPLICANT: The Government of the United States					
APPLICANT: as represented by the Secretary of the					
APPLICANT: Department of Health and Human Services					
TITLE OF INVENTION: Antibodies, Including Fv Molecules, and					
TITLE OF INVENTION: Immunconjugates Having High Binding Affinity for					
TITLE OF INVENTION: Mesothelin and Methods for Their Use					
FILE REFERENCE: 015280-339100US					
CURRENT APPLICATION NUMBER: US/10/973,718					
PRIOR FILING DATE: 2004-10-25					
PRIOR APPLICATION NUMBER: US/09/581,345					
PRIOR FILING DATE: 2000-09-27					
PRIOR APPLICATION NUMBER: US 60/067,175					
PRIOR FILING DATE: 1997-12-01					
PRIOR APPLICATION NUMBER: WO PCT/US98/25270					
PRIOR FILING DATE: 1998-11-25					
NUMBER OF SEQ ID NOS: 9					
SOFTWARE: PatentIn Ver. 2.0					
SEQ ID NO 5					
LENGTH: 241					
TYPE: PRT					
ORGANISM: Artificial Sequence					
FEATURE:					
OTHER INFORMATION: Description of Artificial Sequence:SS scfv					
US-10-973-718-5					
Query Match					
Best Local Similarity 99.8%; Score 1274; DB 5; Length 241;					
Best Local Similarity 99.6%; Pred. No. 1.2e-82;					
Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;					
QY	1	MGVQLQSGPELEKPGASVKLSCKRSGYFGYTMNWKSHGKLEWIGLTPYNGASS	60		
DB	1	MGVQLQSGPELEKPGASVKLSCKRSGYFGYTMNWKSHGKLEWIGLTPYNGASS	60		
QY	61	YNQKRGKATLTVDKSSSTAYMDLLSTSEDSAVYFCARGGVDGPGDYGQGTIVYSS	120		
DB	61	YNQKRGKATLTVDKSSSTAYMDLLSTSEDSAVYFCARGGVDGPGDYGQGTIVYSS	120		
QY	121	GVGSGGGGSGGGSGDIELTQSPAIMSASPEKXTMTCSASSVYMHYQOKSGTSPKR	180		
DB	121	GVGSGGGGSGGGSGDIELTQSPAIMSASPEKXTMTCSASSVYMHYQOKSGTSPKR	180		
QY	181	WIYDPSKLASGVPRFGSGSGNSYSLTISVEAEDDATYVCOOWSGYPLTFGAGTKLEI	240		
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Db      181 WIDTSEKLSGVPGRRSGSGSNNYSLTISVFEADNATYYCQQWSGYPLTFGAGTLEI 240
QY      241 K 241
      241 K 241
Db      241 K 241

RESULT 2
US-10-259-087A-20
; Sequence 20, Application US/10259087A
; Publication No. US20030130190A1
; GENERAL INFORMATION:
; APPLICANT: Vanderbilt University
; APPLICANT: Hallahan, Dennis E
; APPLICANT: Qu, Shihman
; TITLE OF INVENTION: IN VIVO PANNING FOR LIGANDS TO RADIATION-INDUCED MOLECULES
; FILE REFERENCE: 1242/47/2
; CURRENT APPLICATION NUMBER: US/10/259,087A
; CURRENT FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: US 60/328123
; PRIOR FILING DATE: 2001-10-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial antibody ligand number 2
US-10-259-087A-20

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Query Match Similarity      80.4% ; Score 1025.5 ; DB 4 ; length 242 ;
Beet Local Similarity      81.7% ; Pred. No. 5.2e-65 ;
Matches 196 ; Conservative 13 ; Mismatches 30 ; Indels 1 ; Gaps 1

Qy      2 QVQLQSGSELEKPGASVYLSCKASGYSTGYTMANNVKOSHGLFWIGLITPYNGASSY 61
Db      3 QVLTQDSGPELVKPGASVVMSCKASGYFTSTYMHVWKPKPGGLMIGIINYNNGITK 62

Qy      62 NQKPGKATLVYDKSASTAYMDLSTSESAVYPCARGGYDRCGFYWGQGTFTVVS 121
Db      63 NKKFKKALITDKSSTAYMELSLTSDSAVYICARRNGY-ADDYWGQGTFTVVS 121

Qy      122 VGGSGGGSGGGGGSDIELTQSPAIMSASPGKVTMTCSASSSYVMHWYQKSGTSPK 181
Db      122 GGGSGGGSGGGGGSDIELTQSPAIMSASPGKVTITCSASSSYVMHWPGQKGTSPK 181

Qy      182 IYDTSLASGVPRFSGSGSGNSYLTISVEAEADATYYCQMSGYPLTFPAGATKLEIK 241
Db      182 IYGTSLASGVPRFSGSGSGTSLTISMEAEADATYYCQMSGYPLTFPGGTLEIK 241

RESULT 3
US-10-689-006-20
; Sequence 20, Application US/10689006
; Publication No. US20040191249A1
; GENERAL INFORMATION:
; APPLICANT: Vanderbilt University
; APPLICANT: Hallahan, Dennis E
; APPLICANT: Mernaugh, Raymond
; TITLE OF INVENTION: PHAGE ANTIBODIES TO RADIATION-INDUCIBLE NEOANTIGENS
; FILE REFERENCE: 1242/72
; CURRENT APPLICATION NUMBER: US/10/689, 006
; CURRENT FILING DATE: 2003-10-20
; PRIOR APPLICATION NUMBER: US 09/914,605
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 10/259,087
; PRIOR FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 242
; TYPE: PRT

```

ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Artificial antibody ligand number 2
US-10-689-006-20

Query Match 80.4%; Score 1025.5; DB 4; Length 242;
Best Local Similarity 81.7%; Pred. No. 5.2e-65;
Matches 196; Conservative 13; Mismatches 30; Indels 1; Gaps 1;

QY 2 QVQLQQSGPELEKRGASVYKLSCKASGVSPFGYMMYMWVKOSHGKSLIEWIGLITPYNGASGY 61
Db 3 QVQLQQSGPELEKRGASVYKWSCKASGYTFSTYVWVWVKQKPPGQGLENIYINPDGTY 62
QY 62 NQKFRGKATLTVDKSSSTAYMDLSTLSEDSAVYFCARGSDYRGPDPYWGQGTITVTVSSG 121
Db 63 NEKKRGKALITDSSSTAYMELSLTSEDSAVYTCARFENYG-ALDYWGQGTITVTVSSG 121
QY 122 VGGSGGGGGGGGGSDIELTQSPAIMSASPEKRYTMTCSASSYSYVWYVYQOKSGTSPKRW 181
Db 122 GGGSGGGGGGGGGSDIELTQSPAIMSASPEKRYTMTCSASSYSYVWYVYQOKSGTSPKRW 181
QY 182 IYDTSKLASGYPRFSGSGSGNSYSLTSSVEAEADDAITYCCQMSGYLPRFGATKLEIK 241
Db 182 IYGTSNLASGYPRFSGSGSGTSTSLTSSVEAEADDAITYCCQMSGYLPRFGATKLEIK 241

RESULT 4
US-09-808-037-6
Sequence 6, Application US/09808037
Patent No. US20020052311A1
GENERAL INFORMATION:
APPLICANT: SOLOMON, Beke
APPLICANT: HANAN, Eliat
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT AND/OR DIAGNOSIS OF
TITLE OF INVENTION: NEUROLOGICAL DISEASES AND DISORDERS
FILE REFERENCE: SOLOMON-2D
CURRENT APPLICATION NUMBER: US/09/808,037
CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: 09/629,971
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 09/473,653
PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: US 60/152,417
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin version 3.0
SEQ ID NO 6
LENGTH: 239
TYPE: PRT
ORGANISM: Homo sapiens
US-09-808-037-6

Query Match 79.2%; Score 1010.5; DB 3; Length 239;
Best Local Similarity 79.8%; Pred. No. 6e-64;
Matches 194; Conservative 16; Mismatches 26; Indels 7; Gaps 2;

QY 2 QVQLQQSGPELEKRGASVYKLSCKASGVSPFGYMMYMWVKOSHGKSLIEWIGLITPYNGASGY 61
Db 1 QVQLQQSGPELEKRGASVYKWSCKASGVTFSTYVWVWVKQKPPGQGLENIYINPDGTY 60
QY 62 NQKFRGKATLTVDKSSSTAYMDLSTLSEDSAVYFCARG--GYDGRGFDYWGQGTITVTV 118
Db 61 NQKFRGKATLTVDKSSSTAYMELSLTSEDSAVYTCARFENY----FDYWGQGTITVTV 116
QY 119 SSGVGGSGGGGGSDIELTQSPAIMSASPEKRYTMTCSASSYSYVWYVYQOKSGTSP 178
Db 117 SSGGGGGSGGVGGSDIELTQSPAIMSASPEKRYTMTCSASSYSYVWYVYQOKSGTSP 176
QY 179 KRWIYDTSKLASGYPRFSGSGSGNSYSLTSSVEAEADDAITYCCQMSGYLPRFGATKLEIK 238
Db 177 KRWIYDTSKLASGYPRFSGSGSGTSTSLTSSVEAEADDAITYCCQMSGYLPRFGATKLEIK 236
QY 239 EIK 241

Db 237 EIK 239

RESULT 5
US-10-162-889-6
; Sequence 6, Application US/10162889
; Publication No. US20030077252A1
; GENERAL INFORMATION:
; APPLICANT: SOLOMON, Beke
; APPLICANT: HANAN, Elia
; TITLE OF INVENTION: AGENTS AND COMPOSITIONS AND METHODS UTILIZING SAME
; TITLE OF INVENTION: USEFUL IN DIAGNOSING
; TITLE OF INVENTION: AND/OR TREATING OR PREVENTING PLAQUE FORMING DISEASES
; FILE REFERENCE: SOLOMON=28
; CURRENT APPLICATION NUMBER: US/10/162,889
; CURRENT FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US/09/629,971
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 09/473,653
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: US 60/152,417
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-162-889-6

Query Match 79.2%; Score 1010.5; DB 4; Length 239;
Best Local Similarity 79.8%; Pred. No. 6e-64;
Matches 194; Conservative 16; Mismatches 26; Indels 7; Gaps 2;

QY 2 QVQLQSGPELEKPKASVYKLSCKASGYFTGYTMNWKSHGKSLIEWIGLITPYNGASSY 61
DB 1 QVQLQSGALVLRPGVSVKISCKSGSYFTDYAMHWVQSHAKSLIEWIGVISTYTGDA 60
QY 62 NQKFRGKATLVYDKSSSTAYMDLSTSEDSAVYFCARG---GYDGRGPDYWGQTTVTV 118
DB 61 NQKFRGKATLVYDKSSSTAYMDLSTSEDSAVYFCARG---GYDGRGPDYWGQTTVTV 116
QY 119 SSGVGGSGGGGGGGSDIELTQSPAIMSASPGKRYMTCSASSISYMHWTQOKRGTS 178
DB 117 SSGGGGGGGGGGGSDIELTQSPAIMSASPGKRYMTCSASSISYMHWTQOKRGTS 176
QY 179 KRWIDTSKLASGVPRFSGSGSGNSYSLTISVFEADATYTCQOMSGYPLTFGAGTKL 238
DB 177 KRWIDTSKLASGVPRFSGSGSGNSYSLTISVFEADATYTCQOMSGYPLTFGAGTKL 236
QY 239 EIK 241
DB 237 EIK 239

RESULT 6
US-10-384-788-6
; Sequence 6, Application US/10384788
; Publication No. US20040013647A1
; GENERAL INFORMATION:
; APPLICANT: SOLOMON, Beke
; APPLICANT: FRENKEL, Dan
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING A PLAQUE-FORMING DISEASE
; FILE REFERENCE: SOLOMON=2D.2
; CURRENT APPLICATION NUMBER: US/10/384,788
; CURRENT FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: 60/371,735
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 09/808,037
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/830,954
; PRIOR FILING DATE: 2001-06-22

;; PRIOR APPLICATION NUMBER: 10/162,889
;; PRIOR FILING DATE: 2002-06-06
;; PRIOR APPLICATION NUMBER: 09/473,653
;; PRIOR FILING DATE: 1999-12-29
;; PRIOR APPLICATION NUMBER: 09/629,971
;; PRIOR FILING DATE: 2000-07-31
;; PRIOR APPLICATION NUMBER: 60/152,417
;; PRIOR FILING DATE: 1999-09-03
;; PRIOR APPLICATION NUMBER: PCT/IL00/00518
;; PRIOR FILING DATE: 2000-08-31
;; NUMBER OF SEQ ID NOS: 33
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 6
;; LENGTH: 239
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-384-788-6

Query Match 79.2%; Score 1010.5; DB 4; Length 239;
Best Local Similarity 79.8%; Pred. No. 6e-64;
Matches 194; Conservative 16; Mismatches 26; Indels 7; Gaps 2;

QY 2 QVQLQSGPELEKPKASVYKLSCKASGYFTGYTMNWKSHGKSLIEWIGLITPYNGASSY 61
DB 1 QVQLQSGALVLRPGVSVKISCKSGSYFTDYAMHWVQSHAKSLIEWIGVISTYTGDA 60
QY 62 NQKFRGKATLVYDKSSSTAYMDLSTSEDSAVYFCARG---GYDGRGPDYWGQTTVTV 118
DB 61 NQKFRGKATLVYDKSSSTAYMDLSTSEDSAVYFCARG---GYDGRGPDYWGQTTVTV 116
QY 119 SSGVGGSGGGGGGGSDIELTQSPAIMSASPGKRYMTCSASSISYMHWTQOKRGTS 178
DB 117 SSGGGGGGGGGGGSDIELTQSPAIMSASPGKRYMTCSASSISYMHWTQOKRGTS 176
QY 179 KRWIDTSKLASGVPRFSGSGSGNSYSLTISVFEADATYTCQOMSGYPLTFGAGTKL 238
DB 177 KRWIDTSKLASGVPRFSGSGSGNSYSLTISVFEADATYTCQOMSGYPLTFGAGTKL 236
QY 239 EIK 241
DB 237 EIK 239

RESULT 7
US-10-618-856-6
; Sequence 6, Application US/10618856
; Publication No. US20040052766A1
; GENERAL INFORMATION:
; APPLICANT: SOLOMON, Beke
; APPLICANT: FRENKEL, Dan
; TITLE OF INVENTION: IMMUNIZATION AGAINST AMYLOID PLAQUES USING DISPLAY TECHNOLOGY
; FILE REFERENCE: SOLOMON=2A
; CURRENT APPLICATION NUMBER: US/10/618,856
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US/09/473,653A
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: US 60/152,417
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-618-856-6

Query Match 79.2%; Score 1010.5; DB 4; Length 239;
Best Local Similarity 79.8%; Pred. No. 6e-64;
Matches 194; Conservative 16; Mismatches 26; Indels 7; Gaps 2;

QY 2 QVQLQSGPELEKPKASVYKLSCKASGYFTGYTMNWKSHGKSLIEWIGLITPYNGASSY 61
DB 1 QVQLQSGALVLRPGVSVKISCKSGSYFTDYAMHWVQSHAKSLIEWIGVISTYTGDA 60


```
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: nucleic acid encoding scFv antibody 10A
US-10-689-006-24
```

```
Query Match      78.6%; Score 1003; DB 4; Length 261;
Best Local Similarity 80.9%; Pred. No. 2,2e-63;
Matches 195; Conservative 17; Mismatches 27; Indels 2; Gaps 2;
```

```
QY 2 QVQLQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKSHGKSLIEWIGLITPYNGASSY 61
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 QVQLQSGPELVKFGASVKMSCKASGYTFISYVHWKQNGKSLIEWIGLITDPYGGTSY 62
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 62 NQKFRGKATLVDSKSSSTAYMDLSTSEDSAVYFCARGGYDGRGPDYWGQGTITVSSG 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 NQKFRGKATLVDSKSSSTAYITQLKSLTSEDSAVYFCARMDGYG-GFSTWGQGTITVSS 121
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 GVGSGGGGSGGGSDIELTQSPAIMSAPGEKVTMTCSASSSVYHWYQOKSGTSPKR 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 122 GGGSGGGGSGGGSDIELTQSPAIMSATIGEKVTMSCKASSNVKMTWYQOKSGASPKL 181
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 181 WIYDTSKLASGVPRFSGSGSGNSYSLTISSEVAEDDATYTCQOMSGYPLTFAGTLEIK 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 182 WIYTSNLASGVPRFSGSGSGTSYSLTISSEVAEDDATYTCQOFTSSPYTFSGTLEIK 241
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 241 K 241
Db 242 K 242
```

RESULT 11

```
US-10-259-087A-18
; Sequence 18; Application US/10259087A
; Publication No. US20030130190A1
; GENERAL INFORMATION:
; APPLICANT: Vanderbilt University
; APPLICANT: Hallahan, Dennis E
; APPLICANT: Ou, Shidian
; TITLE OF INVENTION: IN VIVO PANNING FOR LIGANDS TO RADIATION-INDUCED MOLECULES
; FILE REFERENCE: 1242/47/2
; CURRENT APPLICATION NUMBER: US/10/259, 087A
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: US 60/328123
; PRIOR FILING DATE: 2001-10-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial antibody ligand number 1
US-10-259-087A-18
```

```
Query Match      77.5%; Score 989.5; DB 4; Length 242;
Best Local Similarity 80.4%; Pred. No. 1.9e-62;
Matches 193; Conservative 14; Mismatches 32; Indels 1; Gaps 1;
```

```
QY 2 QVQLQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKSHGKSLIEWIGLITPYNGASSY 61
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 QVQLQSGALVMPGASVYMSCKASGYTFIDYMHVWKQRPQGLEMIGALIDSDYTSY 62
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 62 NQKFRGKATLVDSKSSSTAYMDLSTSEDSAVYFCARGGYDGRGPDYWGQGTITVSSG 121
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 NQKFRGKATLVDSKSSSTAYMDLSTSEDSAVYFCARGGYDGRGPDYWGQGTITVSSG 121
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 122 VGGSGGGGSGGGSDIELTQSPAIMSAPGEKVTMTCSASSSVYHWYQOKSGTSPKR 181
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 122 GGGSGGGGSGGGSDIELTQSPAIMSATIGEKVTITCRASSSVYHWYQOKSGTSPKR 181
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 182 IYDTSKLASGVPRFSGSGSGNSYSLTISSEVAEDDATYTCQOMSGYPLTFAGTLEIK 241
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 182 IYDTSKLASGVPRFSGSGSGTSYSLTISSEVAEDDATYTCQORSSYPYTFAGTLEIK 241
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

RESULT 12

```
US-10-689-006-18
; Sequence 18; Application US/10689006
; Publication No. US20040191249A1
; GENERAL INFORMATION:
; APPLICANT: Vanderbilt University
; APPLICANT: Hallahan, Dennis E
; APPLICANT: Merzough, Raymond
; TITLE OF INVENTION: PHAGE ANTIBODIES TO RADIATION-INDUCIBLE NEOANTIGENS
; FILE REFERENCE: 1242/72
; CURRENT APPLICATION NUMBER: US/10/689, 006
; PRIOR FILING DATE: 2003-10-20
; PRIOR APPLICATION NUMBER: US 09/914, 605
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 10/259, 087
; PRIOR FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Artificial antibody ligand number 1
US-10-689-006-18
```

```
Query Match      77.5%; Score 989.5; DB 4; Length 242;
Best Local Similarity 80.4%; Pred. No. 1.9e-62;
Matches 193; Conservative 14; Mismatches 32; Indels 1; Gaps 1;
```

```
QY 2 QVQLQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKSHGKSLIEWIGLITPYNGASSY 61
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 QVQLQSGALVMPGASVYMSCKASGYTFIDYMHVWKQRPQGLEMIGALIDSDYTSY 62
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 62 NQKFRGKATLVDSKSSSTAYMDLSTSEDSAVYFCARGGYDGRGPDYWGQGTITVSSG 121
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 NQKFRGKATLVDSKSSSTAYMDLSTSEDSAVYFCARGGYDGRGPDYWGQGTITVSSG 121
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 122 VGGSGGGGSGGGSDIELTQSPAIMSAPGEKVTMTCSASSSVYHWYQOKSGTSPKR 181
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 122 GGGSGGGGSGGGSDIELTQSPAIMSATIGEKVTITCRASSSVYHWYQOKSGTSPKR 181
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 182 IYDTSKLASGVPRFSGSGSGNSYSLTISSEVAEDDATYTCQOMSGYPLTFAGTLEIK 241
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 182 IYDTSKLASGVPRFSGSGSGTSYSLTISSEVAEDDATYTCQORSSYPYTFAGTLEIK 241
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

RESULT 13

```
US-10-682-845-63
; Sequence 63; Application US/10682845
; Publication No. US20040162411A1
; GENERAL INFORMATION:
; APPLICANT: Lanzavecchia, Antonio
; TITLE OF INVENTION: Potent T cell modulating molecules
; FILE REFERENCE: G2296 US
; CURRENT APPLICATION NUMBER: US/10/682, 845
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US 60/419, 149
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: CA 2,403,313
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 492
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: scFv EpcamxCD3 with M4 mutant in anti-CD3 part
US-10-682-845-63
```

Query Match 75.8%; Score 967.5; DB 4; Length 492;
Best Local Similarity 77.3%; Pred. No. 1.4e-60;
Matches 187; Conservative 17; Mismatches 35; Indels 3; Gaps 1;

QY 3 VOLQSGPELEKPGASVVKSCASGYSFTGYTMNWKSHGKSLKLEWIGLITPNYGASSYN 62
DB 245 IKLQSGAEIARPGASVVKSCKTSGTFTRTYTMHWKQRPQGLEWIGYINPSRGYTNYN 304
QY 63 QKFRKATLTVDKSSSTAYMDLSTLSEDSAVYFCARGGYDGR-GPDYWGQGTITVVS-- 120
DB 305 QKFKDKATLTTDKSSSTAYMDLSTLSEDSAVYFCARSDYDHCYCLDYWGQGTITLTVSSVE 364
QY 121 -GVGSGGGGGGGGGSDILTOSPAIMASPEKVTMTCSASSSVSYMMWYQOKSGTSPK 179
DB 365 GSGSGGGGGGGGGVDIQLTOSPAIMASPEKVTMTCRASSSVSYMMWYQOKSGTSPK 424
QY 180 RMIYDTSKLASGVPRFSGSGNSYSLTSSVEAEDDATYCCQWMSNPLTFGAGTKLE 239
DB 425 RMIYDTSKVASGVPRFSGSGSTYSLTSSMEADATYCCQWMSNPLTFGAGTKLE 484
QY 240 IK 241
DB 485 LK 486

RESULT 14
US-10-682-845-79
; Sequence 79, Application US/10682845
; Publication No. US20040162411A1
; GENERAL INFORMATION:
; APPLICANT: Lanzavecchia, Antonio
; TITLE OF INVENTION: Potent T cell modulating molecules
; FILE REFERENCE: G2296 US
; CURRENT APPLICATION NUMBER: US/10/682,845
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US 60/419,149
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: CA 2,403,313
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 79
; LENGTH: 492
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: scFv EPCAMxCD3 with M31 mutant in anti-CD3 part
US-10-682-845-79

Query Match 75.8%; Score 967.5; DB 4; Length 492;
Best Local Similarity 77.8%; Pred. No. 1.4e-60;
Matches 189; Conservative 18; Mismatches 31; Indels 5; Gaps 3;

QY 3 VOLQSGPELEKPGASVVKSCASGYSFTGYTMNWKSHGKSLKLEWIGLITPNYGASSYN 62
DB 245 IKLQSGAEIARPGASVVKSCKTSGTFTRTYTMHWKQRPQGLEWIGYINPSRGYTNYN 304
QY 63 QKFRKATLTVDKSSSTAYMDLSTLSEDSAVYFCARGGYDGR-GPDYWGQGTITVVS-- 120
DB 305 QKFKDKATLTTDKSSSTAYMDLSTLSEDSAVYFCAR-YYEGRYCLDYWGQGTITLTVSSV 363
QY 121 -GVGSGGGGGGGGGSDILTOSPAIMASPEKVTMTCSASSSVSYMMWYQOKSGTSP 178
DB 364 EGSGSGGGGGGGGGVDIQLTOSPAIMASPEKVTMTCRASSSVSYMMWYQOKSGTSP 423
QY 179 RMIYDTSKLASGVPRFSGSGNSYSLTSSVEAEDDATYCCQWMSNPLTFGAGTKL 238
DB 424 RMIYDTSKVASGVPRFSGSGSTYSLTSSMEADATYCCQWMSNPLTFGAGTKL 483
QY 239 IK 241
DB 484 LK 486

RESULT 15
US-10-682-845-83
; Sequence 83, Application US/10682845
; Publication No. US20040162411A1
; GENERAL INFORMATION:
; APPLICANT: Lanzavecchia, Antonio
; TITLE OF INVENTION: Potent T cell modulating molecules
; FILE REFERENCE: G2296 US
; CURRENT APPLICATION NUMBER: US/10/682,845
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US 60/419,149
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: CA 2,403,313
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 83
; LENGTH: 492
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: scFv EPCAMxCD3 with M65 mutant in anti-CD3 part
US-10-682-845-83

Query Match 75.8%; Score 967.5; DB 4; Length 492;
Best Local Similarity 77.3%; Pred. No. 1.4e-60;
Matches 187; Conservative 17; Mismatches 35; Indels 3; Gaps 1;

QY 3 VOLQSGPELEKPGASVVKSCASGYSFTGYTMNWKSHGKSLKLEWIGLITPNYGASSYN 62
DB 245 IKLQSGAEIARPGASVVKSCKTSGTFTRTYTMHWKQRPQGLEWIGYINPSRGYTNYN 304
QY 63 QKFRKATLTVDKSSSTAYMDLSTLSEDSAVYFCARGGYDGR-GPDYWGQGTITVVS-- 120
DB 305 QKFKDKATLTTDKSSSTAYMDLSTLSEDSAVYFCARSDYDHCYCLDYWGQGTITLTVSSVE 364
QY 121 -GVGSGGGGGGGGGSDILTOSPAIMASPEKVTMTCSASSSVSYMMWYQOKSGTSPK 179
DB 365 GSGSGGGGGGGGGVDIQLTOSPAIMASPEKVTMTCRASSSVSYMMWYQOKSGTSPK 424
QY 180 RMIYDTSKLASGVPRFSGSGNSYSLTSSVEAEDDATYCCQWMSNPLTFGAGTKLE 239
DB 425 RMIYDTSKVASGVPRFSGSGSTYSLTSSMEADATYCCQWMSNPLTFGAGTKLE 484
QY 240 IK 241
DB 485 LK 486

Search completed: April 3, 2006, 05:33:08
Job time : 62 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 3, 2006, 05:30:32 ; Search time 45 Seconds
(without alignments)
163.033 Million cell updates/sec

Title: US-09-979-539-1

Perfect score: 1276
Sequence: 1 MGVOLQSGPELEKRGASVK.....COQNSGYPLTFGATKRLK 241

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 180808 seqs, 30441898 residues

Total number of hits satisfying chosen parameters: 180808

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- Published Applications AA New:*
1: /SIDS/prodata/1/pubpa/US08_NEW_PUB pep:*
2: /SIDS/prodata/1/pubpa/US06_NEW_PUB pep:*
3: /SIDS/prodata/1/pubpa/US07_NEW_PUB pep:*
4: /SIDS/prodata/1/pubpa/PCR_NEW_PUB pep:*
5: /SIDS/prodata/1/pubpa/US09_NEW_PUB pep:*
6: /SIDS/prodata/1/pubpa/US10_NEW_PUB pep:*
7: /SIDS/prodata/1/pubpa/US11_NEW_PUB pep:*
8: /SIDS/prodata/1/pubpa/US60_NEW_PUB pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	964.5	75.6	409 6	US-10-503-590A-2 Sequence 2, Appli
2	948	74.3	241 6	US-10-902-546-6 Sequence 6, Appli
3	936	73.4	241 6	US-10-902-546-5 Sequence 5, Appli
4	907	71.1	290 7	US-11-032-773-957 Sequence 957, App
5	907	71.1	319 7	US-11-032-773-955 Sequence 955, App
6	895	70.1	248 6	US-10-512-184-36 Sequence 36, Appl
7	895	70.1	615 6	US-10-512-184-50 Sequence 50, Appl
8	837.5	65.6	543 6	US-10-495-664-3 Sequence 9, Appli
9	832	65.2	237 6	US-10-073-301A-9 Sequence 9, Appli
10	827	65.2	237 7	US-11-203-137-9 Sequence 9, Appli
11	827	64.8	251 7	US-11-054-515-1921 Sequence 1921, Ap
12	827	64.8	251 7	US-11-266-444-1921 Sequence 1921, Ap
13	824.5	64.6	248 7	US-11-054-515-1778 Sequence 1778, Ap
14	824.5	64.6	248 7	US-11-266-444-1778 Sequence 1778, Ap
15	823	64.5	243 6	US-10-537-061-2 Sequence 2, Appli
16	822.5	64.5	250 7	US-11-054-515-932 Sequence 932, App
17	822.5	64.5	250 7	US-11-266-444-932 Sequence 932, App
18	821.5	64.4	248 7	US-11-054-515-1008 Sequence 1008, Ap
19	821.5	64.4	248 7	US-11-266-444-1008 Sequence 1008, Ap
20	819	64.2	245 7	US-11-054-515-1902 Sequence 1902, Ap
21	819	64.2	245 7	US-11-266-444-1902 Sequence 1902, Ap
22	815	63.9	243 7	US-11-054-515-2063 Sequence 2063, Ap
23	815	63.9	243 7	US-11-266-444-2063 Sequence 2063, Ap
24	813.5	63.8	248 7	US-11-054-515-1446 Sequence 1446, Ap
25	813.5	63.8	248 7	US-11-266-444-1446 Sequence 1446, Ap

26	809	63.4	243 6	US-10-537-061-3 Sequence 3, Appli
27	808.5	63.4	248 7	US-11-054-515-1104 Sequence 1104, Ap
28	808.5	63.4	248 7	US-11-266-444-1104 Sequence 1104, Ap
29	808	63.3	241 7	US-11-054-515-1948 Sequence 1948, Ap
30	808	63.3	241 7	US-11-266-444-1948 Sequence 1948, Ap
31	808	63.3	249 7	US-11-054-515-926 Sequence 926, App
32	808	63.3	249 7	US-11-266-444-926 Sequence 926, App
33	808	63.3	277 7	US-11-126-817-54 Sequence 54, Appl
34	804.5	63.0	248 7	US-11-054-515-1771 Sequence 1771, Ap
35	804.5	63.0	248 7	US-11-266-444-1771 Sequence 1771, Ap
36	804	63.0	249 7	US-11-054-515-918 Sequence 918, App
37	804	63.0	249 7	US-11-266-444-918 Sequence 918, App
38	803.5	63.0	248 7	US-11-054-515-1700 Sequence 1700, Ap
39	803.5	63.0	248 7	US-11-266-444-1700 Sequence 1700, Ap
40	803	62.9	249 7	US-11-054-515-919 Sequence 919, App
41	803	62.9	249 7	US-11-266-444-919 Sequence 919, App
42	801	62.8	249 7	US-11-054-515-1635 Sequence 1635, Ap
43	801	62.8	249 7	US-11-266-444-1635 Sequence 1635, Ap
44	800.5	62.7	246 7	US-11-054-515-2062 Sequence 2062, Ap
45	800.5	62.7	246 7	US-11-266-444-2062 Sequence 2062, Ap

ALIGNMENTS

RESULT 1
US-10-503-590A-2
; Sequence 2, Application US/10503590A
; Publication No. US20060062780A1
; GENERAL INFORMATION:
; APPLICANT: ZOECHER, MARCEL
; APPLICANT: DREIER, TORSTEN
; APPLICANT: BAEBERLE, PATRICK
; TITLE OF INVENTION: DE-IMMUNIZED (POLY) PEPTIDE CONSTRUCTS
; FILE REFERENCE: 028622-0134
; CURRENT APPLICATION NUMBER: US/10/503,590A
; CURRENT FILING DATE: 2004-08-12
; PRIOR APPLICATION NUMBER: PCT/EP03/01389
; PRIOR FILING DATE: 2003-02-12
; PRIOR APPLICATION NUMBER: EP 02003332.0
; PRIOR FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 2
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-503-590A-2

Query Match 75.6%; Score 964.5; DB 6; Length 409;
Best Local Similarity 77.3%; Pred. No. 1.5e-56;
Matches 187; Conservative 17; Mismatches 35; Indels 3; Gaps 1;
QY 3 VOLQSGPELEKRGASVYLCKASGSPFTGYTMVWVKGSKLEWIGITPPYNGASSYN 62
DB 162 IKLQSGABLRAPGASVWKSCTSGYTRITMHWKRPQGLFWIGITPPYNGASSYN 221
QY 63 QKFRKATLTVYDKSSSTAYMDLILTSBDAVYFCARGYDGRGPDYWGQGTIVSS-- 120
DB 222 QKFKATLTVYDKSSSTAYMDLILTSBDAVYFCARGYDGRGPDYWGQGTIVSS-- 120
QY 121 -GVGSGGGGGGGGGGSDIELTQSPALMGASGEGKTYMTCSASSSYVMHWYQKSGTSPK 179
DB 282 GGGSGGGGGGGGGGSDIELTQSPALMGASGEGKTYMTCSASSSYVMHWYQKSGTSPK 341
QY 180 RMIYDTSKLAGVPRFSGSGGNSYSLLTISVEAEDATYCCQWMSGYPLTFGAGTKLE 239
DB 342 RMIYDTSKLAGVPRFSGSGGNSYSLLTISVEAEDATYCCQWMSGYPLTFGAGTKLE 401
QY 240 IK 241
DB 402 IK 403

RESULT 2
US-10-902-546-6
; Sequence 6, Application US/10902546
; Publication No. US20060024667A1
; GENERAL INFORMATION:
; APPLICANT: Manucharyan, Karen
; APPLICANT: Gevorgyan, Gohar
; TITLE OF INVENTION: CIP: Compositions and Methods for Alzheimer's Disease
; FILE REFERENCE: new
; CURRENT APPLICATION NUMBER: US/10/902,546
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-902-546-6

Query Match 74.3%; Score 948; DB 6; Length 241;
Best Local Similarity 75.0%; Pred. No. 1,1e-55;
Matches 180; Conservative 25; Mismatches 35; Indels 0; Gaps 0;

QY 2 QVQLQSGPELEKPGASVKLSCKASGYSTGYTMNWKSHGKSLIEWIGLITPYNGASSY 61
DB 1 QVQLQSGPELEKPGASVKLSCKASGYSTGYTMNWKSHGKSLIEWIGLITPYNGASSY 60
QY 62 NQKFRGKATLTVDKSSSTAYMDLSLTSEDSAVYFCARGYDGRGPDYVCGGTITVYSSG 121
DB 61 NEKFKRATLTVDKSSSTAYMDLSLTSEDSAVYFCARGYDGRGPDYVCGGTITVYSSC 120
QY 122 VGGSGGGGGGGSDIELTQSPAIMSASPGKVTMTCSASSSVSYMHWTQOKSGTSPKRW 181
DB 121 GGGSGGGGGGGSDIELTQSPAIMSASPGKVTMTCSASSSVSYMHWTQOKSGTSPRL 180
QY 182 IYDTSKLASGVPRFSGSGSGNSYSLTSSVEAEDDATYTCQOMSGYPLTFGAGTKLEIK 241
DB 181 IYDTSNVAAGVPRFSGSGSGTSTSLTNMEAEADATYTCQOMSGYPTFGGTTKLEIK 240

RESULT 3
US-10-902-546-5
; Sequence 5, Application US/10902546
; Publication No. US20060024667A1
; GENERAL INFORMATION:
; APPLICANT: Manucharyan, Karen
; APPLICANT: Gevorgyan, Gohar
; TITLE OF INVENTION: CIP: Compositions and Methods for Alzheimer's Disease
; FILE REFERENCE: new
; CURRENT APPLICATION NUMBER: US/10/902,546
; CURRENT FILING DATE: 2004-07-29
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-902-546-5

Query Match 73.4%; Score 936; DB 6; Length 241;
Best Local Similarity 73.8%; Pred. No. 6,9e-55;
Matches 177; Conservative 27; Mismatches 36; Indels 0; Gaps 0;

QY 2 QVQLQSGPELEKPGASVKLSCKASGYSTGYTMNWKSHGKSLIEWIGLITPYNGASSY 61
DB 1 QVQLQSGPELEKPGASVKLSCKASGYSTGYTMNWKSHGKSLIEWIGLITPYNGASSY 60
QY 62 NQKFRGKATLTVDKSSSTAYMDLSLTSEDSAVYFCARGYDGRGPDYVCGGTITVYSSG 121

DB 61 NEKFKRATLTVDKSSSTAYMDLSLTSEDSAVYFCARGYDGRGPDYVCGGTITVYSSS 120
QY 122 VGGSGGGGGGGSDIELTQSPAIMSASPGKVTMTCSASSSVSYMHWTQOKSGTSPKRW 181
DB 121 GGGSGGGGGGGSDIELTQSPAIMSASPGKVTMTCSASSSVSYMHWTQOKSGTSPRL 180
QY 182 IYDTSKLASGVPRFSGSGSGNSYSLTSSVEAEDDATYTCQOMSGYPLTFGAGTKLEIK 241
DB 181 IYDTSNVAAGVPRFSGSGSGTSTSLTNMEAEADATYTCQOMSGYPTFGGTTKLEIK 240

RESULT 4
US-11-032-773-957
; Sequence 957, Application US/11032773
; Publication No. US20060018911A1
; GENERAL INFORMATION:
; APPLICANT: Ault-Riche, Dana
; APPLICANT: Levy, Ronald
; TITLE OF INVENTION: DESIGN OF THERAPEUTICS AND THERAPEUTICS
; FILE REFERENCE: 17102-013001 / 1762
; CURRENT APPLICATION NUMBER: US/11/032,773
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 60/536,184
; PRIOR FILING DATE: 2004-01-12
; PRIOR APPLICATION NUMBER: 60/557,591
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 958
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 957
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pBAD S1CS VS His protein sequence
US-11-032-773-957

Query Match 71.1%; Score 907; DB 7; Length 290;
Best Local Similarity 73.8%; Pred. No. 6,4e-53;
Matches 183; Conservative 17; Mismatches 40; Indels 8; Gaps 3;

QY 2 QVQLQSGPELEKPGASVKLSCKASGYSTGYTMNWKSHGKSLIEWIGLITPYNGASSY 61
DB 3 QVQLQSGPELEKPGASVKLSCKASGYSTGYTMNWKSHGKSLIEWIGLITPYNGASSY 62
QY 62 NQKFRGKATLTVDKSSSTAYMDLSLTSEDSAVYFCARG--GYDGRGPDYVCGGTITVYSS 119
DB 63 NEKFKRATLTVDKSSSTAYMDLSLTSEDSAVYFCARG--GYDGRGPDYVCGGTITVYSS 122
QY 120 S-----GVGSGGGGGGGSDIELTQSPAIMSASPGKVTMTCSASSSV--SYMHWTQOK 173
DB 123 SGAGPGGGGGGGGGSDIELTQSPAIMSASPGKVTMTCSASSSVSYMHWTQOK 182
QY 174 SGTSPKRWIYDTSKLASGVPRFSGSGSGNSYSLTSSVEAEDDATYTCQOMSGYPLTFG 233
DB 183 PGSSPKRWIYDTSKLASGVPRFSGSGSGTSTSLTNMEAEADATYTCQOMSGYPLTFG 242
QY 234 AGTKLEIK 241
DB 243 AGTKLEIK 250

RESULT 5
US-11-032-773-955
; Sequence 955, Application US/11032773
; Publication No. US20060018911A1
; GENERAL INFORMATION:
; APPLICANT: Ault-Riche, Dana
; APPLICANT: Levy, Ronald
; TITLE OF INVENTION: DESIGN OF THERAPEUTICS AND THERAPEUTICS
; FILE REFERENCE: 17102-013001 / 1762
; CURRENT APPLICATION NUMBER: US/11/032,773
; CURRENT FILING DATE: 2005-01-11

PRIOR APPLICATION NUMBER: 60/536,184
PRIOR FILING DATE: 2004-01-12
PRIOR APPLICATION NUMBER: 60/557,591
PRIOR FILING DATE: 2004-03-29
NUMBER OF SEQ ID NOS: 958
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 955
LENGTH: 319
TYPE: PRF
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: pBAD S1C5 CD20 His Protein Sequence
US-11-032-773-955

Query Match 71.1%; Score 907; DB 7; Length 319;
Best Local Similarity 73.8%; Pred. No. 6.9e-53;

Matches 183; Conservative 17; Mismatches 40; Indels 8; Gaps 3;

QY 2 QVQLQSGPELEKPKASVYLSCKASGYFTGTYMNMVQSHGKSLIEWIGLITPYNGASSY 61
DB 3 EVQLQSGAEIVKPGASVYKISCKASGYFTDHYIHVKQRPQGLEWIGLITPGNDIRY 62
QY 62 NQKFRKATLTVDKSSSTAYMDLLSTSEDSAVYFCARG--GYDGRGPDYWGQGTITVYS 119
DB 63 NEKFKDKATLTADKSSSTAYMDLNSLTSEDSAVYFCRSPFYDDNYGDYWGQGTITVYS 122
QY 120 S---GVGGSGGGGGGGSDIELTOSPAIMASPEKRYTMTCSASSV--SYMHWYQOK 173
DB 123 SSGAPGGGGGGGGGGSDIYLTQSPAIMASLEERVTMTCTASSSVSSSYFHWYQOK 182
QY 174 SGRSPKRWIYDTSKLAAGVPRFGSGSGNSYSLTISSEADDAITYYCOQMSGPLYTSG 233
DB 183 PSSSPKMTYTTSNLASGVAPRFGSGSGSTISLTISSEADDAITYYCHHRSPITRG 242
QY 234 AGTKLEIK 241
DB 243 AGTKLEIK 250

RESULT 6
US-10-512-184-36
Sequence 36, Application US/10512184
Publication No. US20050244901A1
GENERAL INFORMATION:
APPLICANT: Fraunhofer Gesellschaft zur F"orderung der angewandten Forschung e.V.
TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
FILE REFERENCE: 3581.01US01
CURRENT APPLICATION NUMBER: US/10/512,184
CURRENT FILING DATE: 2004-10-22
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 36
LENGTH: 248
TYPE: PRF
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: scFv SS2 with
OTHER INFORMATION: specificity against Sclerotinia sclerotiorum;
OTHER INFORMATION: originates from Mus musculus.
US-10-512-184-36

Query Match 70.1%; Score 895; DB 6; Length 248;
Best Local Similarity 73.1%; Pred. No. 3.4e-52;

Matches 179; Conservative 20; Mismatches 40; Indels 6; Gaps 3;

QY 2 QVQLQSGPELEKPKASVYLSCKASGYFTGTYMNMVQSHGKSLIEWIGLITPYNGASSY 61
DB 3 QVQLQSGGVTLARPGASVYKISCKASGYFTSYMMHWVQRPQGLEWIGAITPGNSDTSY 62
QY 62 NQKFRKATLTVDKSSSTAYMDLLSTSEDSAVYFCARGGYDGRGPDYWGQGTITVYS 121

DB 63 NQKFRKATLTAVTSTAYMELSSLTNEEDSAVYCTRTDMD-YANDYWGQGTSTVYSSG 121
QY 122 -VGSG-----GGSGGGGGSDIELTOSPAIMASPEKRYTMTCSASSSVSYMHWYQOKSGT 176
DB 122 STSGSGKPGPGEGSTKGADIVLPQSPVIMASPEKRYTMTCSASSSVYIYVYQWKSST 181
QY 177 SPKRWIYDTSKLAAGVPRFGSGSGNSYSLTISSEADDAITYYCOQMSGPLYTSGAGT 236
DB 182 SPKRWIYDTSKLAAGVPRFGSGSGSTISLTISSEADDAITYYCOQMSGPLYTSGAGT 241
QY 237 KLEIK 241
DB 242 KLEIK 246

RESULT 7
US-10-512-184-50
Sequence 50, Application US/10512184
Publication No. US20050244901A1
GENERAL INFORMATION:
APPLICANT: Fraunhofer Gesellschaft zur F"orderung der angewandten Forschung e.V.
TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
FILE REFERENCE: 3581.01US01
CURRENT APPLICATION NUMBER: US/10/512,184
CURRENT FILING DATE: 2004-10-22
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 50
LENGTH: 615
TYPE: PRF
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: fusion protein
OTHER INFORMATION: comprising the leader peptide - chitinase - linker
OTHER INFORMATION: - scFv SS2 - cmc/hisc.
US-10-512-184-50

Query Match 70.1%; Score 895; DB 6; Length 615;
Best Local Similarity 73.1%; Pred. No. 7.4e-52;

Matches 179; Conservative 20; Mismatches 40; Indels 6; Gaps 3;

QY 2 QVQLQSGPELEKPKASVYLSCKASGYFTGTYMNMVQSHGKSLIEWIGLITPYNGASSY 61
DB 344 QVQLQSGGVTLARPGASVYKISCKASGYFTSYMMHWVQRPQGLEWIGAITPGNSDTSY 403
QY 62 NQKFRKATLTVDKSSSTAYMDLLSTSEDSAVYFCARGGYDGRGPDYWGQGTITVYS 121
DB 404 NQKFRKATLTAVTSTAYMELSSLTNEEDSAVYCTRTDMD-YANDYWGQGTSTVYSSG 462
QY 122 -VGSG-----GGSGGGGGSDIELTOSPAIMASPEKRYTMTCSASSSVSYMHWYQOKSGT 176
DB 463 STSGSGKPGPGEGSTKGADIVLPQSPVIMASPEKRYTMTCSASSSVYIYVYQWKSST 522
QY 177 SPKRWIYDTSKLAAGVPRFGSGSGNSYSLTISSEADDAITYYCOQMSGPLYTSGAGT 236
DB 523 SPKRWIYDTSKLAAGVPRFGSGSGSTISLTISSEADDAITYYCOQMSGPLYTSGAGT 582
QY 237 KLEIK 241
DB 583 KLEIK 587

RESULT 8
US-10-495-664-3
Sequence 3, Application US/10495664
Publication No. US2005024416A1

GENERAL INFORMATION:
APPLICANT: JUNG, GUNDRAM
TITLE OF INVENTION: BISPECIFIC ANTI-CD28 ANTIBODY MOLECULE
FILE REFERENCE: 034258-0801
CURRENT APPLICATION NUMBER: US/10/495,664

/ CURRENT FILING DATE: 2004-05-12
/ PRIOR APPLICATION NUMBER: PCT/EP02/12545
/ PRIOR FILING DATE: 2002-11-09
/ PRIOR APPLICATION NUMBER: DE 101 56 482.1
/ PRIOR FILING DATE: 2001-11-12
/ NUMBER OF SEQ ID NOS: 3
/ SOFTWARE: PatentIn Ver. 3.3
/ SEQ ID NO 3
/ LENGTH: 543
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
/ OTHER INFORMATION: protein construct
US-10-495-664-3

Query Match 65.6%; Score 837.5; DB 6; Length 543;
Best Local Similarity 67.6%; Pred. No. 3.9e-48;
Matches 169; Conservative 22; Mismatches 46; Indels 13; Gaps 3;

QY 2 QVQLQSGPELTKPGASVYKLSCKASGYSTGYTMNWVKSHGKSLIEWIGLITPYNGASSY 61
DB 287 QVQLQSGPELVKPGASVYKLSCKASGYSTRSMWVVKRPGQGLEWIGRIYFGDQDINY 346
QY 62 NQKFRGKATLVYDKSSSTAYMDLSTSEDSAVYFCARGG----YDGRGFPYMGQITV 116
DB 347 NQKFRGKATLVADKSSSTAYMVSSSLTSDSAVYFCARGNTVVVPT--MDYMGQGITV 403
QY 117 TVSSGGVGGGGGGGGSDIELTQSPALMSAPGKVTMTCSASSV-----SYMHWYQ 171
DB 404 TVSSGGGGGGGGGGSDIELTQSPALMSAPGKVTMTCSASSVSYDGSFMHWYQ 463
QY 172 QKSTSPKMTIYDTSKLASGVPRFSGSGSNYSLTISVVEADDAITYCOQMSGYPLT 231
DB 464 QKRGQPKLLIYASLSEGVPRFSGSGSRITDFTLIDPEADDAITYCOQNNEDPLT 523
QY 232 FQAGTYLEIK 241
DB 524 FQGGTYLEIK 533

RESULT 9
US-10-073-301A-9
/ Sequence 9, Application US/10073301A
/ Publication No. US20050255101A1
/ GENERAL INFORMATION:
/ APPLICANT: Reiter, Yoram
/ APPLICANT: Denzberg, Galit
/ TITLE OF INVENTION: ANTIBODY HAVING A T-CELL RECEPTOR-LIKE SPECIFICITY, YET HIGHER AFFINITY
/ TITLE OF INVENTION: AND THE USE OF SAME IN THE DETECTION AND TREATMENT OF CANCER, VI
/ FILE REFERENCE: 01/23094
/ CURRENT APPLICATION NUMBER: US/10/073,301A
/ CURRENT FILING DATE: 2002-07-02
/ NUMBER OF SEQ ID NOS: 11
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 9
/ LENGTH: 237
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: GI single chain Fv- recombinant antibody protein sequence
US-10-073-301A-9

Query Match 65.2%; Score 832; DB 6; Length 237;
Best Local Similarity 65.0%; Pred. No. 4.4e-48;
Matches 154; Conservative 36; Mismatches 47; Indels 0; Gaps 0;

QY 2 QVQLQSGPELTKPGASVYKLSCKASGYSTGYTMNWVKSHGKSLIEWIGLITPYNGASSY 61
DB 1 QVQLQSGGGLVYKPGASVYKLSCKASGYSTGYTMNWVKSHGKSLIEWIGLITPYNGASSY 60
QY 62 NQKFRGKATLVYDKSSSTAYMDLSTSEDSAVYFCARGGYDGRGFPYMGQITVYVSSG 121

DB 61 PDVYKGFPTISRDAKNTLYIQMSLSKSDPTAMTYCARGMWEGYFPVWGQGITVYVSSG 120
QY 122 VGSGGGGGGGGSDIELTQSPALMSAPGKVTMTCSASSVSYMHWYQKSGTSPKRW 181
DB 121 GGSGGGGGGGGSDIELTQSPALMSAPGKVTMTCSASSVSYMHWYQKSGTSPKRW 180
QY 182 IYDTSKLASGVPRFSGSGSNYSLTISVVEADDAITYCOQMSGYPLTFGAGTKL 238
DB 181 IYDTSNVAAGVYFRRFSGSGSTSLTINRMEADDAITYCOEWSGYPTFGGQTKL 237

RESULT 10
US-11-203-137-9
/ Sequence 9, Application US/11203137
/ Publication No. US20050287141A1
/ GENERAL INFORMATION:
/ APPLICANT: Reiter, Yoram
/ APPLICANT: Denzberg, Galit
/ TITLE OF INVENTION: ANTIBODY HAVING A T-CELL RECEPTOR-LIKE SPECIFICITY, YET HIGHER AFFINITY
/ TITLE OF INVENTION: AND THE USE OF SAME IN THE DETECTION AND TREATMENT OF CANCER, VI
/ FILE REFERENCE: 30177
/ CURRENT APPLICATION NUMBER: US/11/203,137
/ CURRENT FILING DATE: 2005-08-15
/ NUMBER OF SEQ ID NOS: 11
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 9
/ LENGTH: 237
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: GI single chain Fv- recombinant antibody protein sequence
US-11-203-137-9

Query Match 65.2%; Score 832; DB 7; Length 237;
Best Local Similarity 65.0%; Pred. No. 4.4e-48;
Matches 154; Conservative 36; Mismatches 47; Indels 0; Gaps 0;

QY 2 QVQLQSGPELTKPGASVYKLSCKASGYSTGYTMNWVKSHGKSLIEWIGLITPYNGASSY 61
DB 1 QVQLQSGGGLVYKPGASVYKLSCKASGYSTGYTMNWVKSHGKSLIEWIGLITPYNGASSY 60
QY 62 NQKFRGKATLVYDKSSSTAYMDLSTSEDSAVYFCARGGYDGRGFPVWGQGITVYVSSG 121
DB 61 PDVYKGFPTISRDAKNTLYIQMSLSKSDPTAMTYCARGMWEGYFPVWGQGITVYVSSG 120
QY 122 VGSGGGGGGGGSDIELTQSPALMSAPGKVTMTCSASSVSYMHWYQKSGTSPKRW 181
DB 121 GGSGGGGGGGGSDIELTQSPALMSAPGKVTMTCSASSVSYMHWYQKSGTSPKRW 180
QY 182 IYDTSKLASGVPRFSGSGSNYSLTISVVEADDAITYCOQMSGYPLTFGAGTKL 238
DB 181 IYDTSNVAAGVYFRRFSGSGSTSLTINRMEADDAITYCOEWSGYPTFGGQTKL 237

RESULT 11
US-11-054-515-1921
/ Sequence 1921, Application US/11054515
/ Publication No. US2005025532A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
/ FILE REFERENCE: PFS23P3
/ CURRENT APPLICATION NUMBER: US/11/054,515
/ CURRENT FILING DATE: 2005-02-10
/ PRIOR APPLICATION NUMBER: 60/543,296
/ PRIOR FILING DATE: 2004-02-11
/ PRIOR APPLICATION NUMBER: 60/580,347
/ PRIOR FILING DATE: 2004-06-18
/ PRIOR APPLICATION NUMBER: 10/293,418
/ PRIOR FILING DATE: 2002-11-14
/ PRIOR APPLICATION NUMBER: 60/331,469

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; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1921
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1921

Query Match
Best Local Similarity 64.8%; Score 827; DB 7; Length 251;
Matches 158; Conservative 37; Mismatches 45; Indels 10; Gaps 2;

QY 2 QVQLQSGPELEKPKASVYKLSCKASGYSTGYTMNWVQSHGKSLIEWIGLITPPYNGASSY 61
DB 1 QVQLVQSGAEVKKPKASVYKLSCKASGYFTSYGISWVQARPQGLEMMGWISAINGNTNY 60
QY 62 NQKFRGKATLVYDKSSSTAYMDLSTLSEDSAVYFCAR-----GGYDGRGPDYWGQ 112
DB 61 AOKLGRVTMTDTISTAYMELRSLRSDDTAVYICAVTSLYSSSSGGYYTGGMDVWGR 120
QY 113 GTTVTVSSGVGGSGGGSGGSDIELTQSPALMSAPGEKVTMTCSASSV-SYMWYQ 171
DB 121 GTTVTVSSGGGGSGGGSGGSDIQMTQSPFLSASVGRVITICRASQGINNYLAWYQ 180
QY 172 QKSGTSPKRWIYDTSKLASGVPRGSRGSGNSYSLTSSVBAEDDATYYCOQMGYPIT 231
DB 181 QKGPAPKLLIYAASLSQGVPSRPSGSGGTFDTLTSSLOPEDFATYYCLQDSDDYPLT 240
QY 232 FGAGTKLEIK 241
DB 241 FGGGTKLEIK 250

RESULT 12
US-11-266-444-1921
; Sequence 1921, Application US/11266444
; Publication No. US20060062789A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulatc
; FILE REFERENCE: PF533PID1
; CURRENT APPLICATION NUMBER: US/11/266,444
; PRIOR FILING DATE: 2005-11-04
; PRIOR APPLICATION NUMBER: 09/880,746
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1921
; LENGTH: 251
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-11-266-444-1921

Query Match
Best Local Similarity 64.8%; Score 827; DB 7; Length 251;
Matches 158; Conservative 37; Mismatches 45; Indels 10; Gaps 2;

QY 2 QVQLQSGPELEKPKASVYKLSCKASGYSTGYTMNWVQSHGKSLIEWIGLITPPYNGASSY 61
DB 1 QVQLVQSGAEVKKPKASVYKLSCKASGYFTSYGISWVQARPQGLEMMGWISAINGNTNY 60
QY 62 NQKFRGKATLVYDKSSSTAYMDLSTLSEDSAVYFCAR-----GGYDGRGPDYWGQ 112
DB 61 AOKLGRVTMTDTISTAYMELRSLRSDDTAVYICAVTSLYSSSSGGYYTGGMDVWGR 120
QY 113 GTTVTVSSGVGGSGGGSGGSDIELTQSPALMSAPGEKVTMTCSASSV-SYMWYQ 171
DB 121 GTTVTVSSGGGGSGGGSGGSDIQMTQSPFLSASVGRVITICRASQGINNYLAWYQ 180
QY 172 QKSGTSPKRWIYDTSKLASGVPRGSRGSGNSYSLTSSVBAEDDATYYCOQMGYPIT 231
DB 181 QKGPAPKLLIYAASLSQGVPSRPSGSGGTFDTLTSSLOPEDFATYYCLQDSDDYPLT 240
QY 232 FGAGTKLEIK 241
DB 241 FGGGTKLEIK 250

RESULT 13
US-11-054-515-1778
; Sequence 1778, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1778
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1778

Query Match
Best Local Similarity 64.6%; Score 824.5; DB 7; Length 248;
Matches 156; Conservative 37; Mismatches 47; Indels 7; Gaps 2;

QY 2 QVQLQSGPELEKPKASVYKLSCKASGYSTGYTMNWVQSHGKSLIEWIGLITPPYNGASSY 61
DB 1 QVQLVQSGAEVKKPKASVYKLSCKASGYFTSYGISWVQARPQGLEMMGWISAINGNTNY 60
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[illegible]

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RESULT 14
US-11-266-444-1778
; Sequence 1778, Application US/11266444
; Publication No. US20060062789A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulator
; FILE REFERENCE: PFS23PDI1
; CURRENT FILING DATE: 2005-11-04
; PRIOR APPLICATION NUMBER: US/11/266,444
; PRIOR FILING DATE: 2005-11-04
; PRIOR APPLICATION NUMBER: 09/880,746
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1778
; LENGTH: 248
; TYPE: PRF
; ORGANISM: Homo sapiens
US-11-266-444-1778

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Query Match	64.6%	Score 824.5	DB 7	Length 248
Best Local Similarity	63.2%	Pred. No. 14e-47		
Matches	156	Conservative 37	Mismatches 47	Indels 7
			Gaps	2
QY	2	QVQLQDSGPELEKPGASVYLSCKASGYSFTGYTMNWKVQSHGSKLEWIGLITPYNGASY	61	
Db	1	QVQLQDSGAEVRRKPGASVAVKSCASGYTFTSYGISWVRQAPGHLEEMGMISAYNGNTMY	60	
QY	62	NQKFRGKATLTVDKSSSTAYMDLSTSSDSAVYFCARG-----GYDGRGPDVWGQTT	115	
Db	61	AQKLQGRVMTTDTSTAYMELRSRSDDTAVYCARSYDILITGYVYFPGMDVWGKGTM	120	
QY	116	VTVSSSGVSGSGGGSGGSDIELTQSPALMAGSPERKTYMTCSASSV-STMHVYQOKS	174	
Db	121	VTVSSSGGSGSGGGSGGSDIOMTQSPSLTSSIDRVTITCRASBGLVHMLAWYQOKP	180	
QY	175	GTSPKRWIVDTSKLASGVGRFSGSGSGNSYSLTSSVSAEDATYYCQMGSGPLTFGA	234	
Db	181	GNAPKLLIYKASSLASGAPSRFSGSGSDFTLLTSSLPQDPDAIYYCQQSYNPPLTFEG	240	
QY	235	GTKLEIK 241		
Db	241	GTKLEIK 247		

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RESULT 15
US-10-537-061-2
; Sequence 2, Application US/10537061
; Publication No. US20060051359a1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
; APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
; APPLICANT: HUMAN SERVICES
; APPLICANT: SLOAN-KETTERING INSTITUTE FOR CANCER RESEARCH
; APPLICANT: Pastan, Ira
; APPLICANT: Onda, Masanori
; APPLICANT: Cheung, Nai-Kong
; TITLE OF INVENTION: IN-VIVO CYTOTOXIC ACTIVITIES OF RECOMBINANT IMMUNOTOXIN 8H9
; TITLE OF INVENTION: (FV)-PE88 AGAINST BREAST CANCER, OSTEOCARCINOMA AND NEUROBLASTIC
; FILE REFERENCE: 4239-67287-05
; CURRENT APPLICATION NUMBER: US/10/537, 061
; CURRENT FILING DATE: 2005-06-01
; PRIOR APPLICATION NUMBER: PCT/US03/038227
; PRIOR FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: US 60/430,305
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 243
; TYPE: prt
; ORGANISM: Mus musculus
US-10-537-061-2

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Query Match	64.5%	Score	823	DB	6	Length	243
Best Local Similarity	66.4%	Pred.	N.1.7e-47				
Matches	160	Conservative	29	Mismatches	50	Indels	2
Gap							
QY	2	QYOLQSPPELEKPPASVKLSCKASGYFTGYTMVNMQSHCKSLSEWIGLITPNVNGASSY	61				
DB	1	QVKLQOOSAEELVKKPPASVKLSCKASGYFTNDINWVRBPQGLEWIGLITPPGGSGTOY	60				
QY	62	NQKFRGKATLLTVDKSSSTAYMDLSTLSEDSAVVFCARGYDGRGPDYWGQGTITVTVSSG	121				
DB	61	NEKFRGKATLLTDTSSSTAYMQLSRLTSEDSAVVFCAR-QTATWFAWGCQGTITVTVSSD	119				
QY	122	VGGSGGGGGGGGGSIELTQSPALMASAPGKAVMTGASASSVS-YMNMVQOKSGTSPKR	180				
DB	120	GGGSGGGGGGGGGSIELTQSPFTLSTVPGDVSLSCKASOSISDYLHMVQOKSHSPRL	179				
QY	181	WIYDPSKLASGVPRFSSGSGSNYSLLTSSVEAEDDATYYCQOMSGYPLTFGACTKLEI	240				
DB	180	LIKVASQGISIGIPSRFSGSGGSDPTLINSVPEPDVGYYCQNGHSPFLTFGACTKLEL	239				
QY	241	K 241					
DB	240	K 240					

Search completed: April 3, 2006, 05:31:37
Job time : 46 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 3, 2006, 05:30:14 ; Search time 23 Seconds

(Without alignments)
866.297 Million cell updates/sec

Title: US-09-979-539-1

Sequence: 1 MOVUQSGPELEKFGASVK.....COQMSGYPLTFGATKLEIK 241

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/prodata/1/1aa/5_COMB.pep:.*
2: /cgn2_6/prodata/1/1aa/6_COMB.pep:.*
3: /cgn2_6/prodata/1/1aa/H_COMB.pep:.*
4: /cgn2_6/prodata/1/1aa/PCITUS_COMB.pep:.*
5: /cgn2_6/prodata/1/1aa/RE_COMB.pep:.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1274	99.8	241	2	US-09-581-345-5
2	1010.5	79.2	239	1	US-09-830-954A-6
3	993	77.8	244	1	US-08-553-497A-20
4	987	77.4	242	1	US-08-553-497A-26
5	982.5	77.0	297	2	US-09-486-814A-2
6	981.5	76.9	599	1	US-08-463-163-3
7	979	76.7	244	1	US-08-553-497A-22
8	977	76.5	242	1	US-08-553-497A-28
9	976.5	76.5	239	2	US-08-279-772A-8
10	976.5	76.5	239	2	US-08-902-486-11
11	972	76.2	246	1	US-08-553-497A-24
12	959.5	75.2	256	2	US-09-526-738A-2
13	959.5	75.2	258	2	US-09-526-738A-4
14	956.5	75.0	495	2	US-09-948-004-18
15	908	71.2	238	2	US-09-798-689-21
16	902.5	70.7	246	1	US-08-469-486-57
17	902.5	70.7	246	1	US-08-469-658-57
18	897.5	70.3	264	2	US-10-114-716A-46
19	889.5	69.7	270	1	US-08-652-507-2
20	885.5	69.4	281	2	US-09-423-439-44
21	885.5	69.4	666	2	US-09-423-439-51
22	883.5	69.2	553	1	US-08-661-052-16
23	883.5	69.2	553	1	US-09-188-082-16
24	883.5	69.2	553	2	US-09-364-088-16
25	883.5	69.2	553	2	US-09-102-716-16
26	866	67.9	267	2	US-09-485-737B-2
27	866	67.9	267	2	US-10-071-485-2

28	866	67.9	541	2	US-09-485-737B-85	Sequence 85, Appl
29	866	67.9	541	2	US-10-071-485-85	Sequence 85, Appl
30	866	67.9	711	2	US-09-485-737B-90	Sequence 90, Appl
31	866	67.9	711	2	US-10-071-485-90	Sequence 90, Appl
32	854	66.9	284	2	US-09-184-658-40	Sequence 40, Appl
33	854	66.9	284	2	US-09-504-262D-40	Sequence 40, Appl
34	849.5	66.6	255	2	US-09-553-488-8	Sequence 8, Appl
35	849.5	66.6	255	2	US-09-618-869-8	Sequence 8, Appl
36	841.5	65.9	273	1	US-08-403-853-18	Sequence 18, Appl
37	841	65.9	235	1	US-08-190-159A-61	Sequence 61, Appl
38	839	65.8	267	2	US-09-419-788-30	Sequence 30, Appl
39	834.5	65.4	240	2	US-09-485-737B-91	Sequence 91, Appl
40	834.5	65.4	240	2	US-10-071-485-91	Sequence 91, Appl
41	831.5	65.2	240	1	US-08-800-198-8	Sequence 8, Appl
42	831.5	65.2	240	1	US-09-296-595-8	Sequence 8, Appl
43	829	65.0	288	2	US-09-423-439-38	Sequence 38, Appl
44	829	65.0	673	2	US-09-423-439-32	Sequence 32, Appl
45	823	64.5	260	1	US-08-447-402-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-581-345-5
Sequence 5, Application US/09581345
Patent No. 6809184
GENERAL INFORMATION:
APPLICANT: Pastan, Ira H.
APPLICANT: Chowdhury, Partha S.
APPLICANT: The Government of the United States
APPLICANT: as represented by The Secretary of the
TITLE OF INVENTION: Department of Health and Human Services
TITLE OF INVENTION: Antibodies, including Fv Molecules, and
TITLE OF INVENTION: Immunocjugates Having High Binding Affinity for
FILE REFERENCE: 015280-339100US
CURRENT APPLICATION NUMBER: US/09/581,345
CURRENT FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US 60/067,175
PRIOR FILING DATE: 1997-12-01
PRIOR APPLICATION NUMBER: WO PCT/US98/25270
PRIOR FILING DATE: 1998-11-25
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 5
LENGTH: 241
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: ss scfv
US-09-581-345-5

Query Match	99.8%	Score 1274;	DB 2;	Length 241;
Beet Local Similarity	99.6%	Pred. No. 1.3e-95;		
Matches 240;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MOVUQSGPELEKFGASVKLSCKASGYSFGYTMNWKSHGSLIEWIGLITPNYGSS	60	
DB	1	MOVUQSGPELEKFGASVKLSCKASGYSFGYTMNWKSHGSLIEWIGLITPNYGSS	60	
QY	61	YNQKRGKATLTVDKSSSTAYMDLLSTSEDSAVYFCARGGYDGRGFDYWGQTTVTSS	120	
DB	61	YNQKRGKATLTVDKSSSTAYMDLLSTSEDSAVYFCARGGYDGRGFDYWGQTTVTSS	120	
QY	121	GVGSGGGSGGSDITLTOSPAIMASPEKXTMTCSSSYVMHWYQKSGTSPKR	180	
DB	121	GVGSGGGSGGSDITLTOSPAIMASPEKXTMTCSSSYVMHWYQKSGTSPKR	180	
QY	181	WIYDTSKLASGVPRFSGSGSGNSYSLTSSVEAEADATYCCQMSGYPLTFGATKLEI	240	
DB	181	WIYDTSKLASGVPRFSGSGSGNSYSLTSSVEAEADATYCCQMSGYPLTFGATKLEI	240	

QY 241 K 241
Db 241 K 241

RESULT 2

US-09-830-954A-6
Sequence 6, Application US/09830954A
Patent No. 6919075
GENERAL INFORMATION:
APPLICANT: SOLOMON, Beke
APPLICANT: FRENNEL, Dan
APPLICANT: HANN, Elise
TITLE OF INVENTION: AGENTS AND COMPOSITIONS AND METHODS UTILIZING SAME USEFUL IN DIAG
TITLE OF INVENTION: AND/OR TREATING OR PREVENTING PLAQUE FORMING DISEASES
FILE REFERENCE: SOLOMON-2C
CURRENT APPLICATION NUMBER: US/09/830,954A
CURRENT FILING DATE: 2001-05-03
PRIOR APPLICATION NUMBER: PCT/IL00/00518
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 09/629,971
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 09/473,653
PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: US 60/152,417
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 6
LENGTH: 239
TYPE: PRT
ORGANISM: Homo sapiens
US-09-830-954A-6

Query Match 79.2%; Score 1010.5; DB 2; Length 239;

Best Local Similarity 79.8%; Pred. No. 2,8e-74;
Matches 194; Conservative 16; Mismatches 26; Indels 7; Gaps 2;

QY 2 QVQLQSGPELEKPGASVKISCKASGYFTGYTMNWVKSHGKSLIEWIGLITPYNGASY 61
Db 1 QVQLQSGAEIVKPGASVKISCKSGYFTFDYMHVWVKSHAKSLIEWIGLITPYNGASY 60
QY 62 NQKFRKATLVYDKSSSTAYMDLSTLSEDSAVYFCARG--GYDGRGPDYNGGGTTVTV 118
Db 61 NQKFRKATLVYDKSSSTAYMDLSTLSEDSAVYFCARGTMSY---FDYNGQVTVTV 116
QY 119 SSGVGGSGGGSGGSDIELTQSPAIMSAPGEKVTMTCSASSSYVMHWYQOKSGTSP 178
Db 117 SSGGSGSGVGGSGGSDIELTQSPAIMSAPGEKVTMTCSASSISYVMHWYQOKSGTSP 176
QY 179 KRWIYDTSKLASGVPRFSGSGSGNSYSLTISVSEADDAATYYCCQWMSGYPLTFGAGTKL 238
Db 177 KRWIYDTSKLASGVPRFSGSGSGTSTYSLTISMEADDAATYYCHQRSSYPFTFGGAGTKL 236
QY 239 EIK 241
Db 237 EIK 239

RESULT 3

US-08-553-497A-20
Sequence 20, Application US/08553497A
Patent No. 5844093
GENERAL INFORMATION:
APPLICANT: KETTLERBOROUGH, C. A.
APPLICANT: BENDIG, MARY M.
APPLICANT: ANSELL, KEITH H.
APPLICANT: GUSOW, DETLEF
APPLICANT: ADAM, JAUME
APPLICANT: MITJANS, FRANCESCA
APPLICANT: ROSELL, ELISABET
APPLICANT: BLASCO, FRANCESC
APPLICANT: PILIATS, JAUME

TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZEILANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD, SUITE 1400
CITY: ARLINGTON
STATE: VA
COUNTRY: US
ZIP: 22201

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,497A
FILING DATE: 17-NOV-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP95/00978
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94104160.0
FILING DATE: 17-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94118970.6
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1726
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:
LENGTH: 244 amino acids
TYPE: amino acid
TOPOLOGY: linear

US-08-553-497A-20
MOLLECULE TYPE: protein

Query Match 77.8%; Score 993; DB 1; Length 244;

Best Local Similarity 79.9%; Pred. No. 7.4e-73;
Matches 195; Conservative 14; Mismatches 31; Indels 4; Gaps 2;

QY 2 QVQLQSGPELEKPGASVKISCKASGYFTGYTMNWVKSHGKSLIEWIGLITPYNGASY 61
Db 1 EVQLQSGAEIVKPGASVKISCKSGYFTSHMHVWVKRAGGLEWIGEFNPSGRTNY 60
QY 62 NQKFRKATLVYDKSSSTAYMDLSTLSEDSAVYFCARG--GYDGRGPDYNGGGTTVTVS 119
Db 61 NEKFRKATLVYDKSSSTAYMDLSTLSEDSAVYFCARSDYDGRYDYNGGGTTVTVS 120
QY 120 SSGVGGSGGGSGGSDIELTQSPAIMSAPGEKVTMTCSASSSYVMHWYQOKSGTSPK 179
Db 121 SSGGSGSGGSGGSDIELTQSPAIMSAPGEKVTMTCSASSSYVMHWYQOKSGTSPK 180
QY 180 KRWIYDTSKLASGVPRFSGSGSGNSYSLTISVSEADDAATYYCCQWMSGYPLTFGAGTKL 237
Db 181 LLIYDTSKLASGVPRFSGSGSGTSTYSLTISMEADDAATYYCCQWMSGYPLTFGAGTKL 240
QY 238 LEIK 241
Db 241 LEIK 244

RESULT 4

US-08-553-497A-26
Sequence 26, Application US/08553497A
Patent No. 5844093
GENERAL INFORMATION:

APPLICANT: KETTLERBOROUGH, C. A.
APPLICANT: BENDIG, MARY M.
APPLICANT: ANSELL, KEITH H.
APPLICANT: GUSSON, DELEF
APPLICANT: ADAM, JAUME
APPLICANT: MITJANS, FRANCESCA
APPLICANT: ROSELL, ELISABET
APPLICANT: BLASCO, FRANCESC
APPLICANT: PILATS, JAUME
TITLE OF INVENTION: ANTI-BGFR SINGLE-CHAIN FVS AND ANTI-EGFR
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD. SUITE 1400
CITY: ARLINGTON
STATE: VA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,497A
FILING DATE: 17-NOV-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP95/00978
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94104160.0
FILING DATE: 17-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94118970.6
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1726
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 242 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-553-497A-26

Query Match 77.4%; Score 987; DB 1; Length 242;
Best Local Similarity 79.3%; Pred. No. 2,2e-72;
Matches 192; Conservative 16; Mismatches 32; Indels 2; Gaps 1;

QY 2 QVQLQSGPELEKPGASVTLSCKASGYSTGYTMNWKQSHKSLIEWIGLITPPYGASTY 61
DB 1 QVQLQSGPELEKPGASVTLSCKASGYSTGYTMNWKQSHKSLIEWIGLITPPYGASTY 60

QY 62 NQKFRGKATLVNDKSSSTAYMDLSTSEDSAVYPCARG--GYDRGPGYWGQGTYYVS 119
DB 61 NQKFRGKATLVNDKSSSTAYMDLSTSEDSAVYPCARG--GYDRGPGYWGQGTYYVS 120

QY 120 SGVSGSGGGSGGGSDIELTQSPALMSASPGSKVTMTCSASSSVYMHMYOQKSGTSPK 179
DB 121 SGGSGGGGGGGGGSDIELTQSPALMSASPGSKVTMTCSASSSVYTYWYQKSGTSPK 180

QY 180 RWIYDTSKLASGVPRFGSGSGNSYSLTISVEAEDDATTYCCQWMSGYPLTFGAGTKLE 239
DB 181 LLIYDTSNLAGVPRFGSGSGTSTLISRMEADATYCCQWMSGYPLTFGAGTKLE 240

QY 240 IK 241

DB 241 IK 242

RESULT 5
US-09-486-814A-2
Sequence 2, Application US/09486814A
Patent No. 6562599
GENERAL INFORMATION:
APPLICANT: YAMAMOTO, Masato
APPLICANT: HAYASHI, No. 6562599
APPLICANT: YAMAMOTO, Hiroko
APPLICANT: TOHDOH, Naoki
TITLE OF INVENTION: SINGLE-CHAIN ANTIBODY AGAINST HEPATITIS B VIRUS CORE
TITLE OF INVENTION: PROTEIN, GENE THEREOF, AND THERAPEUTIC AGENT FOR
FILE REFERENCE: 0020-4682P
CURRENT FILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 297
TYPE: PRT
ORGANISM: Mus sp., strain: Balb/c, tissue: spleen
NAME/KEY: PEPTIDE
LOCATION: (1)..(145)
OTHER INFORMATION: Identification Method: P
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (177)..(279)
OTHER INFORMATION: Identification Method: P
US-09-486-814A-2

Query Match 77.0%; Score 982.5; DB 2; Length 297;
Best Local Similarity 78.7%; Pred. No. 6.6e-72;
Matches 192; Conservative 15; Mismatches 28; Indels 9; Gaps 3;

QY 2 QVQLQSGPELEKPGASVTLSCKASGYSTGYTMNWKQSHKSLIEWIGLITPPYGASTY 61
DB 40 QVQLQSGPELEKPGASVTLSCKASGYSTGYTMNWKQSHKSLIEWIGLITPPYGASTY 99

QY 62 NQKFRGKATLVNDKSSSTAYMDLSTSEDSAVYPCARGGYDGRGFDYWGQGTYYVS 121
DB 100 NQKFRGKATLVNDKSSSTAYMDLSTSEDSAVYPCARGGYDGRGFDYWGQGTYYVS 154

QY 122 VGSGGGGSGGGSDIELTQSPALMSASPGSKVTMTCSASSSV--YMHMYOQKSGTSPK 179
DB 155 GGGSGGGGGGGSDIELTQSPALMSASPGSKVTMTCSASSSV--YMHMYOQKSGTSPK 214

QY 180 RWIYDTSKLASGVPRFGSGSGNSYSLTISVEAEDDATTYCCQWMSGY--LTFGAGTK 237
DB 215 LLIYDTSNLAGVPRFGSGSGTSTLISRMEADATYCCQWMSGY--LTFGAGTK 274

QY 238 LEIK 241
DB 275 LEIK 278

RESULT 6
US-08-463-163-3
Sequence 3, Application US/08463163
Patent No. 5696237
GENERAL INFORMATION:
APPLICANT: Fitzgerald, David J.
APPLICANT: Chaudhary, Vijay K.
APPLICANT: Pastan, Ira H.
APPLICANT: Waldmann, Thomas A.
TITLE OF INVENTION: Recombinant Antibody-Toxin Fusion Protein
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stuart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,163
FILING DATE: 05-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/227,227
FILING DATE: 22-JAN-1981
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/911,227
FILING DATE: 24-SEP-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/341,361
FILING DATE: 21-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/865,722
FILING DATE: 08-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen L.
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 015280-12211
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 599 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-463-163-3

Query Match 76.9%; Score 981.5; DB 1; Length 599;

Best Local Similarity 78.8%; Pred. No. 1,8e-71;
Matches 190; Conservative 14; Mismatches 34; Indels 3; Gaps 1;

QY 1 MOVQLQSGPELEKPGASVYLSCKASGYFTGYTMVMVWQSHKSLIEWIGLITPVNGASS 60
DB 1 MOVQLQSGPELEKPGASVYLSCKASGYFTGYTMVMVWQSHKSLIEWIGLITPVNGASS 60
QY 61 YNOKFRGKATLTVDKSSSTAYMDLISLTSEDSAVYFCARGYDGRGFDYWGQGTIVTVSS 120
DB 61 YNOKFRGKATLTVDKSSSTAYMDLISLTSEDSAVYFCARGYDGRGFDYWGQGTIVTVSS 120
QY 121 GVSGSGGGGGGGGSDIELTQSPAIMSASPEKVTMTCSASSSVSYVMHWYQOKSGISPR 180
DB 121 GVSGSGGGGGGGGSDIELTQSPAIMSASPEKVTMTCSASSSVSYVMHWYQOKSGISPR 180
QY 118 GGSGSGGGGGGGGSDIELTQSPAIMSASPEKVTMTCSASSSVSYVMHWYQOKSGISPR 177
DB 118 GGSGSGGGGGGGGSDIELTQSPAIMSASPEKVTMTCSASSSVSYVMHWYQOKSGISPR 177
QY 181 WIYDTKSLASGVPRFSGSGSGSYSLTISVEAEDATYCCQWMSGYP--LTFGAGTKLEI 240
DB 181 WIYDTKSLASGVPRFSGSGSGSYSLTISVEAEDATYCCQWMSGYP--LTFGAGTKLEI 240
QY 241 K 241
DB 238 K 238

RESULT 7
US-08-553-497A-22
; Sequence 22, Application US/08553497A
; Patent No. 5844093
; GENERAL INFORMATION:
; APPLICANT: KETTLERBOROUGH, C. A.

APPLICANT: BENDIG, MARY M.
APPLICANT: ANSELL, KEITH H.
APPLICANT: GUSSOW, DETLEF
APPLICANT: ADAM, JADME
APPLICANT: MITTANS, FRANCESCA
APPLICANT: ROSELL, ELISABET
APPLICANT: BLASCO, FRANCESCA
APPLICANT: PIUTATS, JADME
TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANTIGAN, P.C.
STREET: 2200 CLARENDON BLVD, SUITE 1400
CITY: ARLINGTON
STATE: VA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,497A
FILING DATE: 17-NOV-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP95/00978
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94104160.0
FILING DATE: 17-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94118970.6
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1726
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 244 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-553-497A-22

Query Match 76.7%; Score 979; DB 1; Length 244;

Best Local Similarity 78.7%; Pred. No. 1e-71;
Matches 192; Conservative 15; Mismatches 33; Indels 4; Gaps 2;

QY 2 QVQLQSGPELEKPGASVYLSCKASGYFTGYTMVMVWQSHKSLIEWIGLITPVNGASSY 61
DB 2 QVQLQSGPELEKPGASVYLSCKASGYFTGYTMVMVWQSHKSLIEWIGLITPVNGASSY 61
QY 62 NOKFRGKATLTVDKSSSTAYMDLISLTSEDSAVYFCARG--GYDGRGFDYWGQGTIVTVSS 119
DB 62 NOKFRGKATLTVDKSSSTAYMDLISLTSEDSAVYFCARG--GYDGRGFDYWGQGTIVTVSS 119
QY 61 NEKIRSKATLTVDKSSSTAYMDLISLTSEDSAVYFCARGDYDGRYFDYWGQGTIVTVSS 120
DB 61 NEKIRSKATLTVDKSSSTAYMDLISLTSEDSAVYFCARGDYDGRYFDYWGQGTIVTVSS 120
QY 120 SGVSGGGGGGGGSDIELTQSPAIMSASPEKVTMTCSASSSVSYVMHWYQOKSGISPR 179
DB 120 SGVSGGGGGGGGSDIELTQSPAIMSASPEKVTMTCSASSSVSYVMHWYQOKSGISPR 180
QY 180 RNIYDTKSLASGVPRFSGSGSGSYSLTISVEAEDATYCCQWMSGYP--LTFGAGTK 237
DB 180 RNIYDTKSLASGVPRFSGSGSGSYSLTISVEAEDATYCCQWMSGYP--LTFGAGTK 237
QY 238 LEIK 241
DB 238 LEIK 241


```
RESULT 10
US-08-902-486-11
; Sequence 11, Application US/08902486
; Patent No. 6140075
; GENERAL INFORMATION:
; APPLICANT: Russel, David R.
; APPLICANT: Fuller, James T.
; TITLE OF INVENTION: METHOD FOR PRODUCING ANTIBODIES AND
; TITLE OF INVENTION: PROTEIN TOXINS IN PLANT CELLS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/902,486
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27386
; REFERENCE/DOCKET NUMBER: 670513.90261
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-251-5000
; TELEFAX: 608-251-9166
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-902-486-11

Query Match 76.5%; Score 976.5; DB 2; Length 239;
Best Local Similarity 78.8%; Pred. No. 1.6e-71;
Matches 189; Conservative 14; Mismatches 34; Indels 3; Gaps 1;

QY 2 QVQLQSGPELEKPKASVYKLSCKASGYSTGYTMNWVKOSHGKSLIEWIGLITPPYNGASSY 61
DB 3 QVQLQSGPELEKPKASVYKLSCKASGYSTGYTMNWVKOSHGKSLIEWIGLITPPYNGASSY 62
QY 62 NQKFRGKATLTVDKSSSTAYMDLSTSEDSAVYFCARGGYDGRGPDYWGQGTITVVS 121
DB 63 NQKFRGKATLTVDKSSSTAYMDLSTSEDSAVYFCARGGYDGRGPDYWGQGTITVVS 119
QY 122 VGGSGGGGGGGGSDIELTQSPAIMSASPGKVTMTCSASSSVNHWYQOKSGTSPKRW 181
DB 120 GGGSGGGGGGGGSDIELTQSPAIMSASPGKVTMTCSASSSVNHWYQOKSGTSPKRW 179
QY 182 IYVTSKLASGVPRFGSGSGSNYSLTISSEAEADATYYCOQWSYPTLPFGAGTTLKLIK 241
DB 180 IYVTSKLASGVPRFGSGSGSNYSLTISSEAEADATYYCHORSTYPLTFSGGTTLKLIK 239

RESULT 11
US-08-553-497A-24
; Sequence 24, Application US/08553497A
; Patent No. 5844093
; GENERAL INFORMATION:
; APPLICANT: KETTLERBROUGH, C. A.
; APPLICANT: BENDIG, MARY M.
; APPLICANT: ANSELM, KEITH H.
; APPLICANT: GUSLOW, DETLEF
; APPLICANT: ADAM, JAUME
```

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APPLICANT: MITJANS, FRANCESCA
APPLICANT: ROSELL, ELISABET
APPLICANT: BLASCO, FRANCESCA
APPLICANT: PILATS, JAUME
TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLER, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD, SUITE 1400
CITY: ARLINGTON
STATE: VA
COUNTRY: US
ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/553,497A
; FILING DATE: 17-NOV-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP95/00978
; FILING DATE: 16-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94104160.0
; FILING DATE: 17-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94118970.6
; FILING DATE: 02-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: HAMLET-KING, DIANA
; REGISTRATION NUMBER: 33,302
; REFERENCE/DOCKET NUMBER: MERCK 1726
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-553-497A-24

Query Match 76.2%; Score 972; DB 1; Length 246;
Best Local Similarity 78.5%; Pred. No. 3.7e-71;
Matches 193; Conservative 14; Mismatches 33; Indels 6; Gaps 3;

QY 2 QVQLQSGPELEKPKASVYKLSCKASGYSTGYTMNWVKOSHGKSLIEWIGLITPPYNGASSY 61
DB 1 EVQLQSGPELEKPKASVYKLSCKASGYSTGYTMNWVKOSHGKSLIEWIGLITPPYNGASSY 60
QY 62 NQKFRGKATLTVDKSSSTAYMDLSTSEDSAVYFCARG--GYDGRGPDYWGQGTITVVS 119
DB 61 NQKFRGKATLTVDKSSSTAYMDLSTSEDSAVYFCARGDYDGRGPDYWGQGTITVVS 120
QY 120 SGVSGGGGGGGG--GSDIELTQSPAIMSASPGKVTMTCSASSSVNHWYQOKSGTSPKRW 177
DB 121 SGVSGGGGGGGG--GSDIELTQSPAIMSASPGKVTMTCSASSSVNHWYQOKSGTSPKRW 180
QY 178 PRKWTYVTSKLASGVPRFGSGSGSNYSLTISSEAEADATYYCOQWSYPTLPFGAGTTLKLIK 235
DB 181 PRKWTYVTSKLASGVPRFGSGSGSNYSLTISSEAEADATYYCOQWSYPTLPFGAGTTLKLIK 240
QY 236 TTKLIK 241
DB 241 TTKLIK 246

RESULT 12
```

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US-09-526-738A-2
: Sequence 2, Application US/09526738A
: Patent No. 6630584
: GENERAL INFORMATION:
: APPLICANT: RAMOT UNIVERSITY AUTHORITY FOR APPLIED RESEARCH & INDUSTRIAL DEVELOPMENT
: APPLICANT: LTD.
: TITLE OF INVENTION: SINGLE CHAIN ANTIBODY AGAINST MUTANT P53
: FILE REFERENCE: 1196336
: CURRENT APPLICATION NUMBER: US/09/526,738A
: CURRENT FILING DATE: 2000-03-16
: NUMBER OF SEQ ID NOS: 9
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 2
: LENGTH: 256
: TYPE: PRT
: ORGANISM: Humanus
US-09-526-738A-2

Query Match
Best Local Similarity 75.2%; Score 959.5; DB 2; Length 256;
Matches 187; Conservative 13; Mismatches 36; Indels 5; Gaps 2;

QY 2 QVQLQSGPELEKPGASVKLSCKASGYSTFTYTNMVKQSHGKSLNWIGLITPYNGASST 61
Db 1 QVQLQSGAEIAKPGASVKMSCKTSGYFTSYMMNWKQPGQGLIEWIGINPTGYTKY 60
QY 62 NQKRGKATLTVDKSSSTAYMDLSTLSEDSAVYFCARG-GYDGRGPDYWGQGTITVVS 120
Db 61 NQKFDKATLTADKSSSTAYWQLSLTFTVDASVYYCTGYSTY---FDYWGQGTITVVS 116
QY 121 GVGGSGGGSGGSGSDIELTQSPAIMSASPEKVTMTCSASSSYVHMVQKSGTSPKR 180
Db 117 GGGSGGGSGGSGGSDIELTQSPAIMSASPEKVTITCSASSSYVHMVWFQKPGTSPKL 176
QY 181 WIYPTSKLASGVPRFSGSGSGNSYSLTISVEAEADATYYCCQOMSGYPLTFGAGTKLEI 240
Db 177 WISSTSNLASGVPRFSGSGSGTISLTIISMBAEDATYYCCQRRSSYPTTFGGGTQLQI 236
QY 241 K 241
Db 237 K 237

RESULT 13
US-09-526-738A-4
: Sequence 4, Application US/09526738A
: Patent No. 6630584
: GENERAL INFORMATION:
: APPLICANT: RAMOT UNIVERSITY AUTHORITY FOR APPLIED RESEARCH & INDUSTRIAL DEVELOPMENT
: APPLICANT: LTD.
: TITLE OF INVENTION: SINGLE CHAIN ANTIBODY AGAINST MUTANT P53
: FILE REFERENCE: 1196336
: CURRENT APPLICATION NUMBER: US/09/526,738A
: CURRENT FILING DATE: 2000-03-16
: NUMBER OF SEQ ID NOS: 9
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 4
: LENGTH: 258
: TYPE: PRT
: ORGANISM: Humanus
US-09-526-738A-4

Query Match
Best Local Similarity 75.2%; Score 959.5; DB 2; Length 258;
Matches 187; Conservative 13; Mismatches 36; Indels 5; Gaps 2;

QY 2 QVQLQSGPELEKPGASVKLSCKASGYSTFTYTNMVKQSHGKSLNWIGLITPYNGASST 61
Db 3 QVQLQSGAEIAKPGASVKMSCKTSGYFTSYMMNWKQPGQGLIEWIGINPTGYTKY 62
QY 62 NQKRGKATLTVDKSSSTAYMDLSTLSEDSAVYFCARG-GYDGRGPDYWGQGTITVVS 120
Db 63 NQKRDKATLTADKSSSTAYWQLSLTFTVDASVYYCTGYSTY---FDYWGQGTITVVS 118

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QY      121  GVGGSGGGGGGGSDIELTOSPAITMASPGKMTTCSSASSVSVMHYQOKSGTSPKR 180
Db      119  GGGSGGGGGGGGGSDIELTOSPAITMASPGKMTTCSSASSVSVMHYQOKSGTSPKL 178
QY      181  WIYDTSKLASGVYRFGSGSGGNSYSLTISSEAEADDAITYYCOQMSGVPLTFGAGTKLEI 240
Db      179  WISSTNSNLASGVYRFGSGSGGTSTSLTISRHEADDAITYYCOQSSSYTTFGGGKRLQI 238
QY      241  K 241
Db      239  K 239

RESULT 14
US-09-948-004-18
; Sequence 18, Application US/09948004
; Patent No. 6723538
; GENERAL INFORMATION:
; APPLICANT: MACK, Mathias
; TITLE OF INVENTION: Antibody and/or chemokine constructs and their use in
; FILE REFERENCE: E 2411 EP
; CURRENT APPLICATION NUMBER: US/09/948,004
; CURRENT FILING DATE: 2001-09-05
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 495
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-948-004-18

Query Match      75.0%; Score 956.5; DB 2; Length 495;
Best Local Similarity 76.9%; Pred. No. 1.5e-69;
Matches 186; Conservative 17; Mismatches 36; Indels 3; Gaps 1

QY      3  VOLQOOSGELEKPGASVYLSCKASGYSPFTYTMVWVKOSHGKSLFMIGLITPYNGASSYN 62
Db      248  IKLQOOSGAELARPASVYMSCKTSGYTRITRMHWKORPGGLEIMIGTINFSRGTYNYN 307
QY      63  QKFRGKATLIVDKSSSTAYMDLLSLTSDSAVYFCARGYDGRGPDYWGQGTIVTVSS-- 120
Db      308  QKFRDKATLITDKSSSTAYMDLLSLTSDSAVYFCARYDDHYCLDYWRQGTTLIVSSVSE 367
QY      121  -GVGSGGGGGGGGGSDIELTOSPAITMASPGKMTTCSSASSVSVMHYQOKSGTSPK 179
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QY      180  RWIYDTSKLASGVYRFGSGSGGNSYSLTISSEAEADDAITYYCOQMSGVPLTFGAGTKLE 239
Db      428  RWIYDTSKVASGVYRFGSGSGGTSTSLTISRHEADDAITYYCOQSSSNPLTFGAGTKLE 487
QY      240  IK 241
Db      488  LK 489

RESULT 15
US-09-798-689-21
; Sequence 21, Application US/09798689
; Patent No. 6811779
; GENERAL INFORMATION:
; APPLICANT: Rockwell, Patricia
; APPLICANT: Goldstein, Neil I.
; TITLE OF INVENTION: Method for Reducing Tumor Growth with VEGF Antagonists
; FILE REFERENCE: Sequence Listings 1-41 for 381-25 CIP
; Patent No. 6811779
; CURRENT APPLICATION NUMBER: US/09/798,689
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 09/401,163
; PRIOR FILING DATE: 1999-09-22

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; PRIOR APPLICATION NUMBER: 08/967,113
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 08/706,804
; PRIOR FILING DATE: 1996-09-03
; PRIOR APPLICATION NUMBER: 08/476,533
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/326,552
; PRIOR FILING DATE: 1994-10-20
; PRIOR APPLICATION NUMBER: 08/196,041
; PRIOR FILING DATE: 1994-02-10
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Mouse
US-09-798-689-21

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Query Match 71.2%; Score 908; DB 2; Length 238;
Best Local Similarity 74.0%; Pred. No. 5.4e-66;
Matches 179; Conservative 17; Mismatches 40; Indels 6; Gaps 2;

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QY 2 OVQLQSGPELEKPGASVYKLSCKASGYFTGYTMVWKSHGKSLIEWIGLITPYNGASSY 61
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QY 62 NQKFRGKATLTVDKSSSTA YMDLSTSEDSAVYFCAR--GGYDGRGPDYMGQTTTVS 119
Db 61 APKFOGKATMTADSSSNTAYLQLSLTSEDTAVYVCNAYYGDYEG---YMGQTTTVS 116
QY 120 SGVGGSGGGSGGGSDIELTOSPAIMGASRGEKVTMTCSASSSVSYMMHWQOKGSTSPK 179
Db 117 SGGGSGGGSGGGSDIELTOSPAIMGASRGEKVTMTCSASSSVSYMMHWFOOKGSTSPK 176
QY 180 RWIYDTSKLAGVPGRFSGSGSGNSYSLTSSVEAEDDATYVYCOOMSGYPLTFGAGTKLE 239
Db 177 LMIYTSNLAGVPGRFSGSGSGTSLTSSVEAEDDATYVYCOORSSYPLTFGSGTKLE 236
QY 240 IK 241
Db 237 IK 238

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Search completed: April 3, 2006, 05:41:32
Job time : 24 secs